



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 169142

TO: Ruixiang Li
Location: rem/4D75/4C70
Art Unit: 1646
Friday, July 15, 2005

Case Serial Number: 10/019151

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC-Biotech/ChemLib

159142

mg

From: Li, Ruixiang
Sent: Tuesday, July 12, 2005 7:09 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application No.10/019,151

Please do a standard search on:

SEQ ID NOS: 1-3 against commercial amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

STIC-BIOTECH/CHEMLIB
JUL 13 2005
15:10

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: 3
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: Q2P
WWW/Internet: _____
Other(Specify): _____

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CC sequences. The invention provides polynucleotides (see AAY57943-55) from
 CC foetal brain, adult testis, adult brain, adult kidney and foetal kidney
 CC (all deposited as ATCC 98404), which encode human secreted proteins (see
 CC AAY4720-29). The polynucleotides and proteins are predicted to have
 CC biological activities which would make them suitable for treating,
 CC preventing or ameliorating medical conditions in humans and animals.
 CC although no supporting data are given. Suggested activities include
 CC nutritional, immune stimulating (e.g. as vaccines) or suppressing
 CC activity, haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, and tumour
 CC inhibition activity

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 2; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 IPOLKCVGTAGCDSTPRKVIQCKNGMDGVQVQVECKTDLIAKFGKTVVSCGYBSS 120
 DB 61 IPOLKCVGTAGCDSTPRKVIQCKNGMDGVQVQVECKTDLIAKFGKTVVSCGYBSS 120
 QY 121 EDQVLRSGCGLENYLDYTELGLOKLSGKOHGPAFSFDYYKMSADSCKMSGLITIV 180
 DB 121 EDQVLRSGCGLENYLDYTELGLOKLSGKOHGPAFSFDYYKMSADSCKMSGLITIV 180
 QY 181 VLLGIAFVYVKLFLSDQYSPPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGPONTGH 240
 DB 181 VLLGIAFVYVKLFLSDQYSPPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGPONTGH 240
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 DB 241 GATSGFGSAFTGQCGYENSGPGFWTGLGTGILGLFSGNRATPPSDSWYPSYPSYP 300
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 DB 301 GTWNRAYSPLHSGSGSYVCSNDDTKRTTASGYGGRRR 339

RESULT 2

AAY57943
 ID AAY57943 standard; protein; 339 AA.

XX AAY57943;

XX 23-MAR-2000 (first entry)

XX Human transmembrane protein HTMPN-67.

XX Human transmembrane protein; HTMPN; diagnosis; immunospecific;

XX anti-proliferative; neuroprotective; immune disorder;

XX reproductive disorder; smooth muscle disorder; neurological disorder;

XX gastrointestinal disorder; developmental disorder;

XX cell proliferative disorder.

XX Homo sapiens.

XX MO9961471-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99MO-US011904.

XX 29-MAY-1998; 98US-0087260P.

XX 02-JUL-1998; 98US-0891674P.

XX 02-OCT-1998; 98US-0103954P.

XX 24-NOV-1998; 98US-0108463P.

XX (INCY-) INCTE PHARM INC.

XX Tang YF, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;

XX Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;

XX WPI; 2000-072605/06.

XX N-PSDB; AAY56764.

XX proteins, polynucleotides, vectors, host cells and antibodies used to

XX diagnose, treat or prevent immune, reproductive, smooth muscle,

XX neurological, gastrointestinal, developmental and cell proliferative

XX disorders.

XX Claim 1; Page 166-167; 229pp; English.

XX AAY56764 to AAY56776 encode AAY57877 to AAY57955 which represent human

XX transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The

XX transmembrane protein have immunospecific, antiproliferative and

XX neuroprotective activities. The human transmembrane proteins,

XX polynucleotides encoding them and other compositions and methods from the

XX present invention, can be used for the diagnosis, treatment or prevention

XX of immune, reproductive, smooth muscle, neurological, gastrointestinal,

XX developmental and cell proliferative disorders. The HTMPN's can be used

XX to treat or prevent disorders associated with a decreased expression or

XX activity of HTMPN

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 3; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFLTAGPALGNDPRLMLRDYKALTLYDRYTSRLDP 60
 DB 1 MAACGPGAGYCLLGLHLFLTAGPALGNDPRLMLRDYKALTLYDRYTSRLDP 60
 QY 61 IPOLKCVGTAGCDSTPRKVIQCKNGMDGVQVQVECKTDLIAKFGKTVVSCGYBSS 120
 DB 61 IPOLKCVGTAGCDSTPRKVIQCKNGMDGVQVQVECKTDLIAKFGKTVVSCGYBSS 120
 QY 121 EDQVLRSGCGLENYLDYTELGLOKLSGKOHGPAFSFDYYKMSADSCKMSGLITIV 180
 DB 121 EDQVLRSGCGLENYLDYTELGLOKLSGKOHGPAFSFDYYKMSADSCKMSGLITIV 180
 QY 181 VLLGIAFVYVKLFLSDQYSPPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGPONTGH 240
 DB 181 VLLGIAFVYVKLFLSDQYSPPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGPONTGH 240
 QY 241 GATSGFGSAFTGQCGYENSGPGFWTGLGTGILGLFSGNRATPPSDSWYPSYPSYP 300
 DB 241 GATSGFGSAFTGQCGYENSGPGFWTGLGTGILGLFSGNRATPPSDSWYPSYPSYP 300
 QY 301 GTWNRAYSPLHSGSGSYVCSNDDTKRTTASGYGGRRR 339
 DB 301 GTWNRAYSPLHSGSGSYVCSNDDTKRTTASGYGGRRR 339

RESULT 3

AAY70117
 ID AAY70117 standard; protein; 339 AA.

XX AAY70117;

XX 06-JUN-2000 (first entry)

XX Human ischaemic heart disease associated protein, PGP980.1.

XX ischaemia; heart disease; human; PGP980.1; cardiomyopathy; cardiac;

XX modulator; treat; prevention; diagnosis.

XX Homo sapiens.

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CC sequences. The invention provides polynucleotides (see AAV62746-55) from
CC foetal brain, adult testis, adult brain, adult kidney and foetal kidney
CC (all deposited as ATCC 99404), which encode human secreted proteins (see
CC AAV74720-29). The polynucleotides and proteins are predicted to have
CC biological activities which would make them suitable for treating,
CC preventing or ameliorating medical conditions in humans and animals,
CC although no supporting data are given. Suggested activities include
CC nutritional, immune stimulating (e.g. as vaccine) or suppressing
CC activity, haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemocytic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, and tumour
CC inhibition activity
XX
XX Sequence 339 AA:
SQ
Query Match 100.0%; Score 1879; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 8.6e-162;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDYKALTLHYDRYTSRRLLDP 60
DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDYKALTLHYDRYTSRRLLDP 60
QY 61 IPOLKCVGTAGCDSTYTPKVIQCONKGMGDYDVOMECKTDLDIAVFKGTIVSCGEYESS 120
DB 61 IPOLKCVGTAGCDSTYTPKVIQCONKGMGDYDVOMECKTDLDIAVFKGTIVSCGEYESS 120
QY 121 EDQYVLRGSCGLEBNLDYTELGLQKLKESGKHGFASPSDYKKMSADSCNMSGILITIV 180
DB 121 EDQYVLRGSCGLEBNLDYTELGLQKLKESGKHGFASPSDYKKMSADSCNMSGILITIV 180
QY 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPSHRYORFTNSAGPPPGFSEFTGPONTGH 240
DB 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPSHRYORFTNSAGPPPGFSEFTGPONTGH 240
QY 241 GATSGFSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPPSY 300
DB 241 GATSGFSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPPSY 300
QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
RESULT 2
AA57943
ID AAY57943 standard; protein; 339 AA.
XX
XX AAY57943;
AC
XX
DT 23-MAR-2000 (first entry)
XX
XX Human transmembrane protein HTMPN-67.
DE
XX
XX Human: transmembrane protein; HTMPN, diagnosis; immunospecific;
KM antiproliferative; neuroprotective; immune disorder;
KM reproductive disorder; smooth muscle disorder; neurological disorder;
KM gastrointestinal disorder; developmental disorder;
KM cell proliferative disorder.
XX
XX Homo sapiens.
OS
XX
XX WO9961471-A2.
XX
XX 02-DEC-1999.
PD
XX
XX 28-MAY-1999; 99WO-US011904.
PF
XX
XX 29-MAY-1998; 98US-0087260P.
PR 02-JUL-1998; 98US-0091674P.
PR 02-OCT-1998; 98US-0102954P.
PR 24-NOV-1998; 98US-0109869P.

XX
XX (INCY-) INCYTE PHARM INC.
PA
XX Tang YT, Lal P, Hillman JT, Yue H, Guegler KJ, Corley NC;
XX Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;
XX WPI; 2000-072605/06.
DR N-PSDB; AA256764.
XX
XX Proteins, polynucleotides, vectors, host cells and antibodies used to
PT diagnose, treat or prevent immune, reproductive, smooth muscle,
PT neurological, gastrointestinal, developmental and cell proliferative
PT disorders.
XX
XX Claim 1; Page 166-167; 229pp; English.
PS
XX
XX AA256698 to AA256776 encode AAY57877 to AAY57955 which represent human
CC transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The
CC transmembrane proteins have immunospecific, antiproliferative and
CC neuroprotective activities. The human transmembrane proteins,
CC polynucleotides encoding them and other compositions and methods from the
CC present invention, can be used for the diagnosis, treatment or prevention
CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,
CC developmental and cell proliferative disorders. The HTMPN's can be used
CC to treat or prevent disorders associated with a decreased expression or
CC activity of HTMPN
XX
XX Sequence 339 AA:
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Query Match 100.0%; Score 1879; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 8.6e-162;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDYKALTLHYDRYTSRRLLDP 60
DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDYKALTLHYDRYTSRRLLDP 60
QY 61 IPOLKCVGTAGCDSTYTPKVIQCONKGMGDYDVOMECKTDLDIAVFKGTIVSCGEYESS 120
DB 61 IPOLKCVGTAGCDSTYTPKVIQCONKGMGDYDVOMECKTDLDIAVFKGTIVSCGEYESS 120
QY 121 EDQYVLRGSCGLEBNLDYTELGLQKLKESGKHGFASPSDYKKMSADSCNMSGILITIV 180
DB 121 EDQYVLRGSCGLEBNLDYTELGLQKLKESGKHGFASPSDYKKMSADSCNMSGILITIV 180
QY 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPSHRYORFTNSAGPPPGFSEFTGPONTGH 240
DB 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPSHRYORFTNSAGPPPGFSEFTGPONTGH 240
QY 241 GATSGFSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPPSY 300
DB 241 GATSGFSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPPSY 300
QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
RESULT 3
AAY70117
ID AAY70117 standard; protein; 339 AA.
XX
XX AAY70117;
AC
XX
DT 06-JUN-2000 (first entry)
XX
XX Human ischaemic heart disease associated protein, FGP980.1.
DE
XX
XX Ischaemia; heart disease; human; FGP980.1; cardiomyopathy; cardiac;
KM modulator; treat; prevention; diagnosis.
XX
XX Homo sapiens.
OS

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FH Key Location/Qualifiers
FT Peptide 1..29
FT /label=Signal_sequence
FT Protein 30..339
FT /label=Mature_human_PGP980.1_protein
FT /note="Ischaemic heart disease associated protein"
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XX MO200011942-A1.
XX
XX 09-MAR-2000.
XX
XX 01-SEP-1999; 99WC-US020015.
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XX 01-SEP-1998; 98US-0098683P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Elastasein R;
XX
XX WPI; 2000-237720/20.
XX
XX N-PSDB; AAZ51193.
XX
XX Isolated nucleic acids encoding a proteins that is differentially
XX expressed during ischemic heart disease and ischemic cardiomyopathy,
XX useful for preventing, diagnosing and treating cardiac disease.
XX
XX Claim 14; Page 50-51; 61pp; English.
XX
XX The present amino acid sequence is the human protein designated as
XX PGP980.1, that is differentially expressed in ischaemic heart disorders.
XX PGP980.1 is isolated from human heart cDNA library and is expressed in
XX heart, brain, placenta, lung, skeletal muscle, kidney and pancreas. This
XX sequence is homologous to PGP980.2 protein, but differs at position 66,
XX wherein PGP980.2 has arginine residue. PGP980.1 has cardiant activity.
XX The DNA may be used as probes to detect and quantify homologous sequences
XX in samples. PGP980.1 sequences can be used to identify modulators, that
XX can be used for treatment, diagnosis and prevention of diseases
XX associated with inappropriate expression and activity of the protein,
XX such as ischaemic heart disease and ischaemic cardiomyopathy
XX
XX Sequence 339 AA:
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Query Match 100.0%; Score 1879; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 8, 6e-162;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID AAB18931 standard; protein; 339 AA.
XX
XX AAB18931;
AC
XX 08-FEB-2001 (first entry)
DT
XX
XX A novel polypeptide designated PRO4499.
DE
XX
XX Secreted protein, transmembrane protein; PRO1484; PRO4334; PRO1122;
XX PRO1889; PRO1880; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
XX PRO4352; PRO4380; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
XX PRO4429; PRO4422; tumour; obesity; diabetes;
XX insulinemia; kidney disorder; Bergers disease; nephropathy;
XX Schomlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
XX Crohns disease.
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XX Homo sapiens.
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XX Key Location/Qualifiers
XX Peptide 1..30
XX /note="signal sequence"
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XX Modified-site 68..74
XX /note="N-myristoylation site"
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XX Modified-site 69..75
XX /note="N-myristoylation site"
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XX Modified-site 98..106
XX /note="tyrosine kinase phosphorylation site"
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XX Modified-site 131..137
XX /note="N-myristoylation site"
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XX Domain 171..190
XX /note="transmembrane domain"
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XX Modified-site 172..176
XX /note="N-glycosylation site"
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XX Modified-site 241..247
XX /note="N-myristoylation site"
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XX Modified-site 247..253
XX /note="N-myristoylation site"
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XX Modified-site 266..272
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XX Modified-site 270..276
XX /note="N-myristoylation site"
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XX Modified-site 278..284
XX /note="N-myristoylation site"
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XX Modified-site 312..318
XX /note="N-myristoylation site"
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XX MO200056889-A2.
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XX 28-SEP-2000.
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XX 01-MAR-2000; 2000WC-US005601.
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XX 23-MAR-1999; 99US-0125778P.
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XX 24-MAR-1999; 99US-0125826P.
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XX 31-MAR-1999; 99US-0127035P.
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XX 05-APR-1999; 99US-0127706P.
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XX 21-APR-1999; 99US-0130359P.
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XX 27-APR-1999; 99US-0131291P.
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XX 03-AUG-1999; 99US-0146970P.
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XX 09-DEC-1999; 99US-0170262P.
XX
XX (GENE ) GENENTECH INC.
XX
XX Desnoyers L, Baton DL, Goddard A, Godowski PJ, Gurney AL, Pan J,
XX

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PI Stewart TA, Matanabe CK, Wood WI, Zhang Z;
 XX MPI, 2000-628263/60.
 DR N-PSDB; AAA96358.
 XX
 XX Novel secreted and transmembrane polypeptides useful for diagnosing tumor
 PT in a mammal, for identifying agonists and antagonists of the polypeptide
 PT and for therapeutic use.
 XX
 XX Claim 12, Fig 46; 222pp; English.
 XX
 CC The present sequence represents a secreted or transmembrane polypeptide.
 CC The specification describes polypeptides designated PRO1484, PRO4334,
 CC PRO1322, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
 CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
 CC PRO6030, PRO4430, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
 CC useful for diagnosing tumour in a mammal. The polypeptides, their
 CC agonists and antagonists are useful treating a condition associated with
 CC expression or activity of the polypeptide. Conditions treated include
 CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
 CC capable of inducing proliferation of mammalian kidney mesangial cells and
 CC are therefore useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger's disease or other
 CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,
 CC dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used
 CC to generate transgenic animals for use in development and screening of
 CC therapeutically useful reagents and also for chromosome identification
 CC and tissue typing
 CC
 XX Sequence 339 AA;
 XX
 SQ
 Query Match 100.0%; Score 1879; DB 3; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MAAACGPGAAAGYCLLLGLHLFLITAGPALGMPDPRMLRDVKALTLHYDRYTSRRLLP 60
 QY 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWCKTDLDIAKFKGTIVSCGEYESS 120
 DB 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWCKTDLDIAKFKGTIVSCGEYESS 120
 QY 121 EDGYVLRGSCGLEEYNDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180
 DB 121 EDGYVLRGSCGLEEYNDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180
 QY 122 EDGYVLRGSCGLEEYNDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180
 DB 122 EDGYVLRGSCGLEEYNDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180
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 DB 181 VLLGIAFVVYKCLFLSDGQYSPPPYSEYPPFSRHYQRFNTSAGPPPGFSEFTGQNTGH 240
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 DB 241 GATSGFGSAFTGQGGYENSGPGFMTGLGTGILLGYLFGSNRAATPFSDSWYTPSPSP 300
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 RESULT 5
 AAB19395
 ID AAB19395 standard; protein; 339 AA.
 XX
 AC AAB19395;
 XX
 DT 06-MAR-2001 (first entry)
 XX
 DE Amino acid sequence of a human secreted protein.
 XX
 XX Secreted protein; platelet disorder; stem cell disorder; osteoporosis;
 KM osteoarthritis; burn; incision; ulcer; periodontal disease; neuropathy;
 KM nervous system disease; bone growth; cosmetic plastic surgery;

KM gut protection; gut regeneration; fibrosis; cancer;
 KM bone marrow transplantation.
 XX
 OS Homo sapiens.
 XX
 PN WO200061755-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 10-APR-2000; 2000MO-US009555.
 XX
 PR 09-APR-1999; 99US-0128574P.
 PR 20-AUG-1999; 99US-0150054P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Garcia PD;
 XX
 DR MPI; 2000-665133/64.
 DR N-PSDB; AAC61881.
 XX
 XX Claim 14; Page 56; 74pp; English.
 CC AAB19395-B19407 represent secreted human proteins. The secreted proteins
 CC are useful in assays to determine their biological activities. The
 CC proteins can also be used as biomarkers to identify tissues or cell types
 CC which express the proteins. The polynucleotide molecules can be used as
 CC biomarkers for tissues or chromosomes and to elicit immune responses. The
 CC proteins and antibodies are useful in diagnosis and treatment of diseases
 CC associated with altered expression of these proteins. The proteins are
 CC also useful for prevention or treatment of platelet disorders, stem cell
 CC disorders, osteoporosis or osteoarthritis, burns, incisions, ulcers,
 CC periodontal diseases, central and peripheral nervous system diseases and
 CC neuropathies, for healing fractured bones and to induce cartilage and/or
 CC bone growth in cosmetic plastic surgery. The proteins are also useful for
 CC gut protection or regeneration, for the treatment of lung or liver
 CC fibrosis, for stimulating blood cell generation in patients receiving
 CC cancer chemotherapy and for treatment of bone marrow transplantation
 CC patients
 CC
 XX Sequence 339 AA;
 XX
 SQ
 Query Match 100.0%; Score 1879; DB 3; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAACGPGAAAGYCLLLGLHLFLITAGPALGMPDPRMLRDVKALTLHYDRYTSRRLLP 60
 DB 1 MAAACGPGAAAGYCLLLGLHLFLITAGPALGMPDPRMLRDVKALTLHYDRYTSRRLLP 60
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 DB 61 IPOLKCVGTAGCDSTTPKVIQCONKGMGDYDVQWCKTDLDIAKFKGTIVSCGEYESS 120
 QY 121 EDGYVLRGSCGLEEYNDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180
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 DB 122 EDGYVLRGSCGLEEYNDYTELGLOKLKESGKHGFASFSYIYKMSADSCKMSGLITTV 180
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 DB 181 VLLGIAFVVYKCLFLSDGQYSPPPYSEYPPFSRHYQRFNTSAGPPPGFSEFTGQNTGH 240
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RESULT 6

AAB20090
ID AAB20090 standard; protein; 339 AA.

AC AAB20090;

DT 23-APR-2001 (first entry)

DE Human hydrophobic domain-containing protein HP03342.

XX Human; hydrophobic domain; antiinflammatory; immunosuppressive;

KW immunostimulant; vulnerric; antitumor; haemostatic; cytostatic;

KW hepatotropic; thrombolytic; antitumor; antiviral; antibacterial;

KW antifungal; gene therapy; diagnosis; membrane protein; secretion.

XX Homo sapiens.

PN MO200100824-A2.

PD 04-JAN-2001.

PF 16-JUN-2000; 2000MO-JP003944.

PR 24-JUN-1999; 99JP-00178065.

XX (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

XX Kato S, Kilmura T;

PI WPI, 2001-123008/13.

DR N-PSDB; AAF30021.

XX New proteins with hydrophobic domains, useful for treating autoimmune

PT diseases, inflammatory diseases, wounds, burns, incisions and ulcers.

XX Claim 1; Page 87-89; 126pp; English.

XX The present sequence is that of a novel human protein having a putative N
CC -terminal secretory and transmembrane domain. It is predicted from cDNA
CC clone HP03342 (see AAF30021). Isolated from a human umbilical cord blood
CC cDNA library. The protein shows sequence similarity to Caenorhabditis
CC elegans hypothetical protein CAA88972. The invention provides human
CC proteins (see AAB20089-96) having hydrophobic domains indicative of
CC secretory signals or membrane domains, and nucleic acids (see AAF30020-
CC 27) encoding them. These are expected to have cell proliferation, cell
CC differentiation, immunostimulant or immunosuppressor, haematopoiesis
CC regulating, tissue growth, activin, inhibin, chemotactic, chemokinetic,
CC haemostatic, thrombolytic, receptor/ligand, antiinflammatory or
CC antitumor activities (no evidence provided). Expression vectors,
CC eukaryotic host cells and antibodies are also provided. The secreted or
CC antigenic proteins of the invention can be used as pharmaceuticals or
CC for preparing antibodies. Cells expressing them are utilized for
CC detection of corresponding receptors or ligands, and in candidate drug
CC screening

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 4; Length 339;

Best Local Similarity 100.0%; Pred. No. 8.6e-162;

Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGAGYCLILGLHLPLTAGPAGMNPDRMLADYKALTLHYRYYTSRLDP 60

DB 1 MAACGPGAGAGYCLILGLHLPLTAGPAGMNPDRMLADYKALTLHYRYYTSRLDP 60

QY 61 IPOLKCVGAGTCDSTYTPKVIQCCKNGWDYDVQWCKTDLDAVYKGTVCCEGYESS 120

DB 61 IPOLKCVGAGTCDSTYTPKVIQCCKNGWDYDVQWCKTDLDAVYKGTVCCEGYESS 120

QY 121 BDQYVARGSGCLEYVNDYTELGLQKLKESKQGFASFSDYYTKMSADSCKNSGLITTV 180

DB 121 BDQYVARGSGCLEYVNDYTELGLQKLKESKQGFASFSDYYTKMSADSCKNSGLITTV 180

QY 181 VILGIAFVYTKFLSPGQISPPPYSEYPPSHRYQRTNSAGPPPGFKEFTGPONTGH 240

DB 181 VILGIAFVYTKFLSPGQISPPPYSEYPPSHRYQRTNSAGPPPGFKEFTGPONTGH 240

QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGGLIGYLFGRNRAATPPSDSWYPSYP 300

DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGGLIGYLFGRNRAATPPSDSWYPSYP 300

QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTASGYGTRRR 339

DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTASGYGTRRR 339

RESULT 7

AAM78498
ID AAM78498 standard; protein; 339 AA.

AC AAM78498;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1160.

XX Human; cytokines; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation.

XX Homo sapiens.

PN MO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001MO-US004098.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

XX (HYSR-) HYSRQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;

DR WPI, 2001-476283/51.

DR N-PSDB; AAK51631.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful

PT in diagnosis and gene therapy.

XX Claim 20; Page 3398-3399; 6221pp; English.

PS The invention relates to polynucleotides (AAK51456-AAK53435) and the

CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to

CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and

CC activity/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111

CC (AAKS2582) and 3666 (AAM60020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 339 AA;
 Query Match 100.0%; Score 1879; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDMMLRDVKALTLHYDRYTSRRLLP 60
 DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDMMLRDVKALTLHYDRYTSRRLLP 60
 QY 61 IPOLKCVGAGTGDSTYTPKVIQCKNGMDGYDVQWCKCTDLDAIFKGTIVSCGEYSS 120
 DB 61 IPOLKCVGAGTGDSTYTPKVIQCKNGMDGYDVQWCKCTDLDAIFKGTIVSCGEYSS 120
 QY 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 DB 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 QY 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 DB 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 QY 181 VLLGIAFVYVKLFLSDGQYSPPPSYSPPSHRYPFTNSAGPPPGFKSEFTGPQNTGH 240
 DB 181 VLLGIAFVYVKLFLSDGQYSPPPSYSPPSHRYPFTNSAGPPPGFKSEFTGPQNTGH 240
 QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGILGYLFGSNRAATPSDSMTYSPSPSY 300
 DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGILGYLFGSNRAATPSDSMTYSPSPSY 300
 QY 301 GTMNRAVSPPLHGGSSGSYSVCSNSDITKRTRTASGYGTRRR 339
 DB 301 GTMNRAVSPPLHGGSSGSYSVCSNSDITKRTRTASGYGTRRR 339

RESULT 8
 AAU29275
 ID AAU29275 standard; protein; 339 AA.
 XX
 AC AAU29275;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #252.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.
 PN WO200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006520.
 XX
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 06-MAR-2000; 2000US-0186968P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 15-MAR-2000; 2000US-0189328P.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 30-MAR-2000; 2000US-0193053P.
 PR 04-APR-2000; 2000US-0194449P.

PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PA (GENTH) GENENTECH INC.
 XX
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-602746/68.
 DR N-PSDB; AAS46176.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 PS Claim 11; Fig 504; 774pp; English.
 XX
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX
 SQ Sequence 339 AA;
 Query Match 100.0%; Score 1879; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.6e-162;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDMMLRDVKALTLHYDRYTSRRLLP 60
 DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDMMLRDVKALTLHYDRYTSRRLLP 60
 QY 61 IPOLKCVGAGTGDSTYTPKVIQCKNGMDGYDVQWCKCTDLDAIFKGTIVSCGEYSS 120
 DB 61 IPOLKCVGAGTGDSTYTPKVIQCKNGMDGYDVQWCKCTDLDAIFKGTIVSCGEYSS 120
 QY 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 DB 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180

QY 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPSHRYQRPFTNSAGPPPGKSEFTGPONTGH 240
 DB 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPSHRYQRPFTNSAGPPPGKSEFTGPONTGH 240
 QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGGIILYLFSGNRAATPPSDSWYTPSPSP 300
 DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGGIILYLFSGNRAATPPSDSWYTPSPSP 300
 QY 301 GTWNRAYSPLHGGSGSYVCSNSDPTKTRTASGVGSTRR 339
 DB 301 GTWNRAYSPLHGGSGSYVCSNSDPTKTRTASGVGSTRR 339
 RESULT 9
 ABB84979
 ID ABB84979 standard; protein; 339 AA.
 AC ABB84979;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO4499 protein sequence SEQ ID NO:326.
 XX
 KW Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;
 KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US019692.
 XX
 PR 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222659P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023322.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-0064610.
 PR 18-SEP-2000; 2000US-0065350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.

PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Matarabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-090516/12.
 DR N-PSDB; ABL88234.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 326; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic, antiangiogenic, hypotensive, vulnary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, CC proteins, agonists and antagonists are useful for treating or diagnosing CC cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration, CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound CC healing. The PRO polynucleotides have applications in molecular biology, CC including use as hybridization probes, and in chromosome and gene CC mapping. ABL88259 to ABL88267 represent primers and probes used in the CC exemplification of the present invention
 XX
 SQ Sequence 339 AA;
 XX
 Query Match 100.0%; Score 1879; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8 6e-162;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAACGPGAAAGYCLLGLHLFLITAGPALGMDPRLMDVAKLTLYADRYTTSRLDP 60
 DB 1 MAAACGPGAAAGYCLLGLHLFLITAGPALGMDPRLMDVAKLTLYADRYTTSRLDP 60
 QY 61 IPQLKCVGGTAGCDSTTPKVIQCONKMGQYDVQMECTDLDIAYKFKTVSCGEYESS 120
 DB 61 IPQLKCVGGTAGCDSTTPKVIQCONKMGQYDVQMECTDLDIAYKFKTVSCGEYESS 120
 QY 121 BDQYVLRGSGGLEYNLDYRELGLQKLKESGKHGFPASFSYXXKWSADSNNSGILITV 180
 DB 121 BDQYVLRGSGGLEYNLDYRELGLQKLKESGKHGFPASFSYXXKWSADSNNSGILITV 180
 QY 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPSHRYQRPFTNSAGPPPGKSEFTGPONTGH 240
 DB 181 VLLGIAFVYVKLFLSDGQYSPPEYSEYPPSHRYQRPFTNSAGPPPGKSEFTGPONTGH 240
 QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGGIILYLFSGNRAATPPSDSWYTPSPSP 300
 DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGGIILYLFSGNRAATPPSDSWYTPSPSP 300
 QY 301 GTWNRAYSPLHGGSGSYVCSNSDPTKTRTASGVGSTRR 339
 DB 301 GTWNRAYSPLHGGSGSYVCSNSDPTKTRTASGVGSTRR 339
 RESULT 10
 ABB61425
 ID ABB61425 standard; protein; 339 AA.
 AC ABB61425;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human NF-kB activating protein SEQ ID NO 3.

CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention
 XX

Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.6e-162; Indels 0; Gaps 0;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAACGPAAGYCLILGLHLFLITAGPALGWNDDPDMRLRDVKALTLHYDRYTSRRLLDP 60
 DB 1 MAAACGPAAGYCLILGLHLFLITAGPALGWNDDPDMRLRDVKALTLHYDRYTSRRLLDP 60
 QY 61 IPOLKCVGTAGCDSTTPKVIQCONKMGDGYDVQMECKTDIDIAVKEGKTIVSCGEYESS 120
 DB 61 IPOLKCVGTAGCDSTTPKVIQCONKMGDGYDVQMECKTDIDIAVKEGKTIVSCGEYESS 120
 QY 121 EDQVYVLAGSGGLEYNLDYTELGLQKLKESGKHQHPASRDYTYKMSGMSGMLTIV 180
 DB 121 EDQVYVLAGSGGLEYNLDYTELGLQKLKESGKHQHPASRDYTYKMSGMSGMLTIV 180
 QY 181 VLLGIAFYVYKLFPLSDQVSPPYSEYPPFSHRVQFTNSAGPPPGFKSEFTGPONTGH 240
 DB 181 VLLGIAFYVYKLFPLSDQVSPPYSEYPPFSHRVQFTNSAGPPPGFKSEFTGPONTGH 240
 QY 241 GATSGFSAFTGQGGYENSGPFWTGLGTGGILGLFGSNRAATPFSDSWYTPSPSY 300
 DB 241 GATSGFSAFTGQGGYENSGPFWTGLGTGGILGLFGSNRAATPFSDSWYTPSPSY 300
 QY 301 GTWNRAYSPLHGSGSYVCNSDTRKTRTASGYGCTRR 339
 DB 301 GTWNRAYSPLHGSGSYVCNSDTRKTRTASGYGCTRR 339

RESULT 12

ABBS5585
 ID ABBS5585 standard; protein; 339 AA.

AC ABB95585;
 DT 19-JUL-2002 (first entry)

XX Human angiogenesis related protein PRO4499 SEQ ID NO: 326.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.

XX Homo sapiens.

XX WO200208284-A2.

PD 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US021735.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-022064P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-0064365P.

PR 23-AUG-2000; 2000WO-US023322.

PR 24-AUG-2000; 2000US-02023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-0064610.

PR 18-SEP-2000; 2000US-0066350.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032578.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001US-0017800.
 PR 20-JUN-2001; 2001WO-US019692.

PA (BETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (BERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODD/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (HARS/) MASTERS S A.
 PA (PANU/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI; 2002-171999/22.
 DR N-PSDB; ABL95723.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 326; 567pp; English.

PS The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention

XX Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.6e-162; Indels 0; Gaps 0;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAACGPAAGYCLILGLHLFLITAGPALGWNDDPDMRLRDVKALTLHYDRYTSRRLLDP 60
 DB 1 MAAACGPAAGYCLILGLHLFLITAGPALGWNDDPDMRLRDVKALTLHYDRYTSRRLLDP 60
 QY 61 IPOLKCVGTAGCDSTTPKVIQCONKMGDGYDVQMECKTDIDIAVKEGKTIVSCGEYESS 120

DB 61 IPOLKCVGAGTACDSDYTPKVIQCONKGMWDYDVQWECKTDLDAVYFKGVSCGEYESS 120
 QY 121 EDQYVLRSGCGLEBNLDYTELGIQKLKESGKHGFASFSFYTKMSADSCKMSGLITTV 180
 DB 121 EDQYVLRSGCGLEBNLDYTELGIQKLKESGKHGFASFSFYTKMSADSCKMSGLITTV 180
 QY 181 VLLGIAFVVYVKLF.LSDGQYSPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGQNTGH 240
 DB 181 VLLGIAFVVYVKLF.LSDGQYSPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGQNTGH 240
 QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGIIIGYLFPSNRATPPSDSWYTPSPSP 300
 DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGIIIGYLFPSNRATPPSDSWYTPSPSP 300
 QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTASGYGTRRR 339
 DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTASGYGTRRR 339

RESULT 13

ABP61841
 ID ABP61841 standard; protein; 339 AA.
 AC ABP61841;
 DT 04-OCT-2002 (first entry)
 DE Human polypeptide SEQ ID NO 195.

XX Human; cytostatic; antirheumatic; antiarthritic; vulnery; analgesic;
 KW antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
 KW neuroprotective; nootropic; osteopathic; haemostatic; vasoconstrictor;
 KW anticancer; fungicide; antidiabetic; antiaesthetic; antiallergic;
 KW immunostimulant; antiparasitic; secreted protein; transmembrane protein;
 KW cytokine; cell proliferation; cell differentiation; autoimmune disease;
 KW stem cell; growth factor; nervous system disease; neuropathy;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
 KW osteoporosis; severe combined immunodeficiency; SCID; infection;
 KW multiple sclerosis; rheumatoid arthritis; gene therapy.

OS Homo sapiens.
 XX US2002065394-A1.
 XX 30-MAY-2002.
 XX 22-DEC-2000; 2000US-00745763.
 XX 18-MAR-1998; 98US-00040963.
 XX (JACO/) JACOBS K.
 PA (MCCO/) MCCOY J M.
 PA (LAVA/) LAVALLIE E R.
 PA (COLL/) COLLINS-RACIE L A.
 PA (EVAN/) EVANS C.
 PA (MERB/) MERBERG D.
 PA (TREAC/) TREACY M.
 PA (SPAUD/) SPAULDING V.
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Spaulding V;
 DR MPI: 2002-582343/62.
 DR N-PSDB; AB092055.
 XX Novel secreted or transmembrane protein and polynucleotide encoding the
 PT protein, useful for diagnosis and treatment of neurological disorders,
 PT cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.
 PS Claim 184; Page 193; 284pp; English.
 XX The invention relates to human secreted or transmembrane protein (I),
 CC

CC their fragments and is encoded by specific complementary deoxyribonucleic
 CC acid (cDNA) inserts (II), where the protein is substantially free from
 CC other mammalian proteins. (I) are useful for preventing, treating or
 CC ameliorating a medical condition, especially immunological treatment or
 CC prevention of tumors. (I) exhibits activity relating to angiogenesis,
 CC cytokine, cell proliferation, cell differentiation, antiinflammatory,
 CC stem cell growth factor activity and activin or inhibin-related
 CC activities. (I) can be used to manipulate stem cells in culture to give
 CC rise to neuroepithelial cells that can be used to augment or replace
 CC cells damaged by illness, autoimmune disease, accidental damage or
 CC genetic disorders. (I) induces the proliferation of neural cells and
 CC regeneration of nerve and brain tissue and is useful for the treatment of
 CC central and peripheral nervous system diseases and neuropathies, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or
 CC periodontal disease. (I) is also useful for gut protection or
 CC regeneration and treatment of lung or liver fibrosis, reperfusion injury
 CC in various tissues, various immune deficiencies and disorders including
 CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
 CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
 CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,
 CC such as asthma or other respiratory problems. (II) is useful to express
 CC recombinant protein, as markers for tissues in which the corresponding
 CC protein is preferentially expressed and in gene therapy. The present
 CC sequence is that of a polypeptide of the invention

Sequence 339 AA;

Query Match 100.0%; Score 1879; DB 5; Length 339;

Best Local Similarity 100.0%; Pred. No. 8.6e-162; Indels 0; Gaps 0;

Matches 339; Conservative 0; Mismatches 0;

QY 1 MAACGPGAGYCLLGLHLFTLTAGPALGMWDPPRMLLRDVKALTLHYDRYTSRRIDP 60
 DB 1 MAACGPGAGYCLLGLHLFTLTAGPALGMWDPPRMLLRDVKALTLHYDRYTSRRIDP 60
 QY 61 IPOLKCVGAGTACDSDYTPKVIQCONKGMWDYDVQWECKTDLDAVYFKGVSCGEYESS 120
 DB 61 IPOLKCVGAGTACDSDYTPKVIQCONKGMWDYDVQWECKTDLDAVYFKGVSCGEYESS 120
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 DB 121 EDQYVLRSGCGLEBNLDYTELGIQKLKESGKHGFASFSFYTKMSADSCKMSGLITTV 180
 QY 181 VLLGIAFVVYVKLF.LSDGQYSPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGQNTGH 240
 DB 181 VLLGIAFVVYVKLF.LSDGQYSPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGQNTGH 240
 QY 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGIIIGYLFPSNRATPPSDSWYTPSPSP 300
 DB 241 GATSGFGSAFTGQGGYENSGPGFWTGLGTGIIIGYLFPSNRATPPSDSWYTPSPSP 300
 QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTASGYGTRRR 339
 DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKRTASGYGTRRR 339

RESULT 14

ABU58651
 ID ABU58651 standard; protein; 339 AA.

XX ABU58651;
 AC 15-APR-2003 (first entry)
 DT Human PRO polypeptide #252.
 DE Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
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KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADDEPT;
KW antibody-dependent enzyme mediated prodruug therapy.
OS Homo sapiens.
XX US2003027272-A1.
XX 06-FEB-2003.
PD
XX
XX 21-JUN-2002; 2002US-00176492.
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PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 06-OCT-1998; 98US-0103258P.
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PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1879; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 8,6e-162;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGCYCLLGLHIFLLTAGPALGMDPDRLADVYKALTLHYDRYTTSRLLDP 60
DB 1 MAACGPGAGCYCLLGLHIFLLTAGPALGMDPDRLADVYKALTLHYDRYTTSRLLDP 60
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DB 61 IPOLKCVGAGTACDSTYTPKVIQCONKGMDDYDVQMECKTDLDAYKFKTIVGCEGYESS 120
QY 121 EDQYVIRGSCGLEBYNDYTELGIQKLKESGKHGFASPSDYIYKMSADSCKNSGLITIV 180
DB 121 EDQYVIRGSCGLEBYNDYTELGIQKLKESGKHGFASPSDYIYKMSADSCKNSGLITIV 180
QY 181 VLLGLAFVYVKFLSPGQVSPPPYSEPPSHYQRTNAGPPPGPSEFTGPQNTGH 240
DB 181 VLLGLAFVYVKFLSPGQVSPPPYSEPPSHYQRTNAGPPPGPSEFTGPQNTGH 240
QY 241 GATSGFGSALFTGQOGYENSGPGFWTGLGTGILGLYFGSNRAATPDSWYTPSPSY 300
DB 241 GATSGFGSALFTGQOGYENSGPGFWTGLGTGILGLYFGSNRAATPDSWYTPSPSY 300
QY 301 GTWNRAYSPLHGGSGSYVCSNSDYTEKRTNAGYGTGTRR 339
DB 301 GTWNRAYSPLHGGSGSYVCSNSDYTEKRTNAGYGTGTRR 339

RESULT 15
ABU88199
ID ABU88199 standard; protein; 339 AA.
XX
AC ABU88199;
XX
DT 07-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4499.
XX
KW Human; secreted and transmembrane protein: PRO; gene therapy;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
XX
PR 18-SRP-1997; 97US-0059263P.
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PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
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PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
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PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
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PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102655P.
PR 06-OCT-1998; 98US-0103258P.

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Best Local Similarity 0; Pred No. 8, 6e-162;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Job time : 120.621 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 20:16:41 ; Search time 102.864 Seconds
(without alignments)
1273.204 Million cell updates/sec

Title: US-10-019-151C-2

Perfect score: 1879

Sequence: 1 MAACGCGAAGYCLLGLHL.....CSNEDTKRTTASGVGTRRR 339

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 38632138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1879	100.0	339	10 US-09-931-836-80	Sequence 80, App1
3	1879	100.0	339	13 US-10-036-342-80	Sequence 80, App1
4	1879	100.0	339	13 US-10-052-585-504	Sequence 504, App
5	1879	100.0	339	13 US-10-036-041-80	Sequence 80, App1
6	1879	100.0	339	14 US-10-035-855-80	Sequence 80, App1
7	1879	100.0	339	14 US-10-174-590-504	Sequence 504, App
8	1879	100.0	339	14 US-10-176-758-504	Sequence 504, App
9	1879	100.0	339	14 US-10-175-737-504	Sequence 504, App
10	1879	100.0	339	14 US-10-174-581-504	Sequence 504, App
11	1879	100.0	339	14 US-10-176-483-504	Sequence 504, App

12	1879	100.0	339	14 US-10-176-749-504	Sequence 504, App
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37	1879	100.0	339	14 US-10-176-992-504	Sequence 504, App
38	1879	100.0	339	14 US-10-176-993-504	Sequence 504, App
39	1879	100.0	339	14 US-10-184-658-504	Sequence 504, App
40	1879	100.0	339	14 US-10-176-921-504	Sequence 504, App
41	1879	100.0	339	14 US-10-036-214-80	Sequence 80, App1
42	1879	100.0	339	14 US-10-173-695-504	Sequence 504, App
43	1879	100.0	339	14 US-10-173-697-504	Sequence 504, App
44	1879	100.0	339	14 US-10-173-705-504	Sequence 504, App
45	1879	100.0	339	14 US-10-174-576-504	Sequence 504, App

ALIGNMENTS

RESULT 1
US-09-745-763-146
Sequence 146, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
McCoy, John M.
Lavallee, Edward R.
Collins-Racle, Lisa A.
Evans, Cheryl
Weber, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.

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/      REGISTRATION NUMBER: 41,323
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: (617) 498-8284
/      TELEFAX: (617) 876-5851
/      INFORMATION FOR SEQ ID NO: 146:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 339 amino acids
/      TYPE: amino acid
/      STRANDEDNESS: <unknown>
/      TOPOLOGY: linear
/      MOLECULE TYPE: protein
/      SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-745-763-146

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DB      181 VLLGIAPVYVKLFLSPDQYSPPPYSEYPPSHRYQRTNSAGPPPPGKSEFTGPQNTGH 240
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/      Publication No. US20030027249A1
/      GENERAL INFORMATION:
/      APPLICANT: Desnoyers, Luc
/      APPLICANT: Baton, Dan L.
/      APPLICANT: Goddard, Audrey
/      APPLICANT: Godowski, Paul J.
/      APPLICANT: Gurney, Austin L.
/      APPLICANT: Pan, James
/      APPLICANT: Stewart, Timothy A.
/      APPLICANT: Watanabe, Colin K.
/      APPLICANT: Wood, William I.
/      APPLICANT: Zhang, Zhenlin
/      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/      FILE REFERENCE: P3030R1C1
/      CURRENT APPLICATION NUMBER: US/09/931,836
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1 PRIOR FILING DATE: 2001-06-29
1 PRIOR APPLICATION NUMBER: PCT/US01/21735
1 PRIOR FILING DATE: 2001-07-09
1 NUMBER OF SEQ ID NOS: 80
1 SEQ ID NO 80
1 LENGTH: 339
1 TYPE: PRT
1 ORGANISM: Homo Sapien
US-09-931-836-80

Query Match 100.0%; Score 1879; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;

Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MAACGPGAGYCLLGLLH.FLLTAGPALGMDPDRMLADVXALTLHYRYYTSRLDP 60
DB 1 IPOLKVVGGTAGCDSTTPKVIQCONKMDGYDVQWEKTLDLAYKRGTVVSCGEGYSS 120
61 IPOLKVVGGTAGCDSTTPKVIQCONKMDGYDVQWEKTLDLAYKRGTVVSCGEGYSS 120
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DB 121 EDOYVLRGSGCLFYNLDYTELGLQKLSGKHGFASFDDYKMSADSCKNSGLITTV 180
121 EDOYVLRGSGCLFYNLDYTELGLQKLSGKHGFASFDDYKMSADSCKNSGLITTV 180
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DB 181 VLLGIAFVVYKFLPSDQYSPPPYSRHYQRTNSAGPPPGFKSEFTGPQNTGH 240
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RESULT 3
US-10-036-342-80

1 Sequence 80, Application US/10036342
1 Publication No. US20020090681A1

1 GENERAL INFORMATION:

1 APPLICANT: Desnoyers, Luc
1 APPLICANT: Batton, Dan L.
1 APPLICANT: Goddard, Audrey
1 APPLICANT: Godowski, Paul J.
1 APPLICANT: Gurney, Austin L.
1 APPLICANT: Pan, James
1 APPLICANT: Stewart, Timothy A.
1 APPLICANT: Watanabe, Colin K.
1 APPLICANT: Wood, William I.

1 APPLICANT: Zhang, Zhenli
1 TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
1 FILE REFERENCES: P3030R1C5
1 CURRENT APPLICATION NUMBER: US/10/036,342
1 PRIOR FILING DATE: 2001-12-26
1 PRIOR APPLICATION NUMBER: 60/085579
1 PRIOR FILING DATE: 1998-05-15
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1 PRIOR APPLICATION NUMBER: 09/644848
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/ PRIOR APPLICATION NUMBER: 09/869599
/ PRIOR FILING DATE: 2001-06-29
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/ PRIOR APPLICATION NUMBER: PCT/US01/19692
/ PRIOR FILING DATE: 2001-06-20
/ PRIOR APPLICATION NUMBER: PCT/US01/21066
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: PCT/US01/21735
/ PRIOR FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 80
/ SEQ ID NO 80
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-036-342-80

Query Match      100.0%; Score 1879; DB 13; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
US-10-052-586-504
/ Sequence 504, Application US/10052586
/ Publication No. US20020127584A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C1
/ CURRENT APPLICATION NUMBER: US/10/052, 586
/ CURRENT FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
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/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089908

Query Match 100.0%; Score 1879; DB 13; Length 339;
Best Local Similarity 100.0%; Pred. No. 46-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 IPOLKCYGAGTACDSTTPKVIQCQNGMDGYDVQMECKTDLDIAYKFGKTVSCBEGYSS 120
Db 61 IPOLKCYGAGTACDSTTPKVIQCQNGMDGYDVQMECKTDLDIAYKFGKTVSCBEGYSS 120

Qy 121 BDQYVVRGSGLEYNLDYRELGIQKLKESGKOHGFASPSDYVYKMSADSNNSGLITIV 180
Db 121 BDQYVVRGSGLEYNLDYRELGIQKLKESGKOHGFASPSDYVYKMSADSNNSGLITIV 180

Db 121 EBOYVLRGSCGLEYNLDYTELGQKESGKHGFASPSDYKWSADSNNMSGILITV 180
QY 181 VLLGLAFVYKLEPLSDGQSPPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGPONTG 240
Db 181 VLLGLAFVYKLEPLSDGQSPPPYSEYPPSHRYORFTNSAGPPPGFKSEFTGPONTG 240
QY 241 GATSGFSAFTGQOQYENSGPGFWTGLGTGILGTYFGSNRATPPSDSNYPSYPSY 300
Db 241 GATSGFSAFTGQOQYENSGPGFWTGLGTGILGTYFGSNRATPPSDSNYPSYPSY 300
QY 301 GTWNRAYSPLHGSGSYSVCSNDTTRTNAGYGTRRR 339
Db 301 GTWNRAYSPLHGSGSYSVCSNDTTRTNAGYGTRRR 339

RESULT 5
US-10-036-041-80
Sequence 80, Application US/10036041
GENERAL INFORMATION:
APPLICANT: Debnover, Inc
APPLICANT: Bacon, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C8
CURRENT APPLICATION NUMBER: US/10/036,041
CURRENT FILING DATE: 2001-12-26
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PRIOR FILING DATE: 2001-06-01
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PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21725
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 80
LENGTH: 339
TYPE: PRT
ORGANISM: Homo Sapien

US-10-036-041-80

Query Match	100.0%;	Score 1879;	DB 13;	Length 339;
Best Local Similarity	100.0%;	Pred. No. 4e-165;		
Matches 339;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy	61 IPOLKCYGTAAGCDSTTPKVIQCCKNGMDGYDVMECKTDLIAVFGKTVASCGEYSS	120
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Qy	121 EDOVYLKSGSGLENTLDYTELGQKLKESGKHGFAPSDYKKMSADSCMSGLTIIV	180
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Qy	121 EDOVYLKSGSGLENTLDYTELGQKLKESGKHGFAPSDYKKMSADSCMSGLTIIV	180
Db	121 EDOVYLKSGSGLENTLDYTELGQKLKESGKHGFAPSDYKKMSADSCMSGLTIIV	180
Qy	181 VLLGLAFVYTKLFLSDGQISPPPYSEYPPPSHRQRFTNSAGPPPGKSEFTGPQNTGH	240
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RESULT 6
US-10-035-855-80

Sequence 80, Application US/10035855
Publication No. US20030008348A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C4
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? PRIOR FILING DATE: 2001-02-28
? PRIOR APPLICATION NUMBER: PCT/US01/17800
? PRIOR FILING DATE: 2001-06-01
? PRIOR APPLICATION NUMBER: PCT/US01/19692
? PRIOR FILING DATE: 2001-06-20
? PRIOR APPLICATION NUMBER: PCT/US01/21066
? PRIOR FILING DATE: 2001-06-29
? PRIOR APPLICATION NUMBER: PCT/US01/21735
? PRIOR FILING DATE: 2001-07-09
? NUMBER OF SEQ ID NOS: 80
? SEQ ID NO 80
? LENGTH: 339
? TYPE: PRT
? ORGANISM: Homo Sapien
US-10-035-855-80

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Query Match	100.0%;	Score 1879;	DB 14;	Length 339;
Best Local Similarity	100.0%;	Pred. No. 4e-165;		
Matches 339;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MAAAGCPAAGACLLLGHLFLTTGPPALGMNDPRLMLPVLKALTLYBDDYTTSRRLDP	60
Db	1	MAAAGCPAAGACLLLGHLFLTTGPPALGMNDPRLMLPVLKALTLYBDDYTTSRRLDP	60
QY	61	IPQLKCVGATAGCDSYTPKVI IQCNKMGDGYDVOMEKCTDLDAIAKFKGTAVSCGEYSS	120
Db	61	IPQLKCVGATAGCDSYTPKVI IQCNKMGDGYDVOMEKCTDLDAIAKFKGTAVSCGEYSS	120
QY	121	EDQVYLRSGCGLENYLADYTELGLOLKRSGQKHGASPSDYIYKMSADSCNMSGLITTV	180
Db	121	EDQVYLRSGCGLENYLADYTELGLOLKRSGQKHGASPSDYIYKMSADSCNMSGLITTV	180
QY	181	VLLGIAFVYVKLFPLSDQGYSPPPYSEYDPFSHRYORFTNSAGPAPPDGGKSEBFTGQNTGH	240
Db	181	VLLGIAFVYVKLFPLSDQGYSPPPYSEYDPFSHRYORFTNSAGPAPPDGGKSEBFTGQNTGH	240
QY	241	GATSGFSGAFLTGQOQYENSGPGFMGLGTGGLIGVLPFSNAAAPFSSSWYIYPSYPPYYP	300
Db	241	GATSGFSGAFLTGQOQYENSGPGFMGLGTGGLIGVLPFSNAAAPFSSSWYIYPSYPPYYP	300
QY	301	GTWNRAVSPPLHGGSGSYVSCNSDPTKRTTASGCGGTRRR	339
Db	301	GTWNRAVSPPLHGGSGSYVSCNSDPTKRTTASGCGGTRRR	339

```

RESULT 7
US-10-174-590-504
; Sequence 504, Application US/10174590
; Publication No. US2003008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 504
; LENGTH: 339
; TYPE: PRRT
;

```

ORGANISM: Homo Sapien
US-10-174-590-504

Query Match	100.0%;	Score 1879;	DB 14;	Length 339;
Best Local Similarity	100.0%;	Pred. NO. 4e-15;		
Matches 339;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	MAAAGCPAAGAYCILLGLHLELTLTGPAALGMNMDPRMLLRVKALTLTYHDTYTSRRLLDP	60
Db	1	MAAAGCPAAGAYCILLGLHLELTLTGPAALGMNMDPRMLLRVKALTLTYHDTYTSRRLLDP	60
QY			
Db			
QY	61	IPOLKCVGSGTACGDSYTPKVIQQCKNGMDGVDMVECKTDLDAIKFEGTVVSGCGYSS	120
Db	61	IPOLKCVGSGTACGDSYTPKVIQQCKNGMDGVDMVECKTDLDAIKFEGTVVSGCGYSS	120
QY	121	EDQVYLRSGCGLEAYLDYTELGLOQLAKESGQKHGAFSESDYYVKKMSADSCKMSGLITIV	180
Db	121	EDQVYLRSGCGLEAYLDYTELGLOQLAKESGQKHGAFSESDYYVKKMSADSCKMSGLITIV	180
QY			
Db			
QY	181	VLLGLIAFVYTKLFSLDQGYSPPPYSEYPPFSHRVORFVNSAGAPPPPGKSEFTGQNTGH	240
Db	181	VLLGLIAFVYTKLFSLDQGYSPPPYSEYPPFSHRVORFVNSAGAPPPPGKSEFTGQNTGH	240
QY	241	GATSGFGSAGTGGQCYENSGPGFWTGLGTGILGLVFGSNNAAATPFSSDWTYPSYPPSY	300
Db	241	GATSGFGSAGTGGQCYENSGPGFWTGLGTGILGLVFGSNNAAATPFSSDWTYPSYPPSY	300
QY	301	GTNNRAYSPLHGGSGSYVSCNSDTKTPTTASGYGGTTRR	339
Db	301	GTNNRAYSPLHGGSGSYVSCNSDTKTPTTASGYGGTTRR	339

RESULT 8
US-10-176-758-504

```

: Sequence 504, Application ID: US10176758
: Publication No. US20030008353A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Deenoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3430R1C104
: CURRENT APPLICATION NUMBER: US/10/176,758
: CURRENT FILING DATE: 2002-06-21
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 504
: LENGTH: 339
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-10-176-758-504

```

Query Match	100.0%;	Score 1879;	DB 14;	Length 339;
Best Local Similarity	100.0%;	Pred. No. 4e-165;		
Matches 339;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 AAAAGCPAAGCULLGHLFLTTAGPALGNNDPGRMLRDVKALTLHYDRYTSRRLLDP 60

Db 1 MAAGGCPAAGCULLGHLFLTTAGPALGNNDPGRMLRDVKALTLHYDRYTSRRLLDP 60

QY 61 IPOLKCVGATGCDSTPRKVIQCKNGKGDYDVQMECTDLDAVFGKTVSCSGYSS 120

Db 61 IPOLKCVGATGCDSTPRKVIQCKNGKGDYDVQMECTDLDAVFGKTVSCSGYSS 120

QY 121 EDQYVLAGSGCGLFYNLDYTELGLQKLKESGKHGFAPSPDYKYKMSADSQNMGLITIV 180
DB 121 EDQYVLAGSGCGLFYNLDYTELGLQKLKESGKHGFAPSPDYKYKMSADSQNMGLITIV 180
QY 181 VLLGIAFVYVKLFLSDQYSPPPYSEYPPFSHRVQRFNTSAGPPPGKSEFTGPONTGH 240
DB 181 VLLGIAFVYVKLFLSDQYSPPPYSEYPPFSHRVQRFNTSAGPPPGKSEFTGPONTGH 240
QY 241 GATSGFSAFTGQGGYENSGPGFMTGTGTGIIIGYLRGSNNAATPFSDSWYTPSPSY 300
DB 241 GATSGFSAFTGQGGYENSGPGFMTGTGTGIIIGYLRGSNNAATPFSDSWYTPSPSY 300
QY 301 GTMNRAYSPLHGGSGSYVCSNPDYKTRTASGYGTTRR 339
DB 301 GTMNRAYSPLHGGSGSYVCSNPDYKTRTASGYGTTRR 339

RESULT 9

US-10-175-737-504
Sequence 504, Application US/10175737
Publication No. US20030013153A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Deenoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C50
CURRENT APPLICATION NUMBER: US/10/175, 737
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 504
LENGTH: 339
TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-737-504

Query Match 100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAACGFGAAGYCLLGLHLFLTAGPAGCNDPDRMLLDVXALTLHYDRYTTSRRLDP 60
DB 1 MAACGFGAAGYCLLGLHLFLTAGPAGCNDPDRMLLDVXALTLHYDRYTTSRRLDP 60
QY 61 IPOLKCVGAGAGCDSTYPRKIYQCONKMGDGYDVQMEKTDLDIAKKGKTVSGEGRESS 120
DB 61 IPOLKCVGAGAGCDSTYPRKIYQCONKMGDGYDVQMEKTDLDIAKKGKTVSGEGRESS 120
QY 121 EDQYVLAGSGCGLFYNLDYTELGLQKLKESGKHGFAPSPDYKYKMSADSQNMGLITIV 180
DB 121 EDQYVLAGSGCGLFYNLDYTELGLQKLKESGKHGFAPSPDYKYKMSADSQNMGLITIV 180
QY 181 VLLGIAFVYVKLFLSDQYSPPPYSEYPPFSHRVQRFNTSAGPPPGKSEFTGPONTGH 240
DB 181 VLLGIAFVYVKLFLSDQYSPPPYSEYPPFSHRVQRFNTSAGPPPGKSEFTGPONTGH 240
QY 241 GATSGFSAFTGQGGYENSGPGFMTGTGTGIIIGYLRGSNNAATPFSDSWYTPSPSY 300
DB 241 GATSGFSAFTGQGGYENSGPGFMTGTGTGIIIGYLRGSNNAATPFSDSWYTPSPSY 300
QY 301 GTMNRAYSPLHGGSGSYVCSNPDYKTRTASGYGTTRR 339
DB 301 GTMNRAYSPLHGGSGSYVCSNPDYKTRTASGYGTTRR 339

RESULT 10

US-10-174-581-504
Sequence 504, Application US/10174581
Publication No. US20030017540A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Deenoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C41
CURRENT APPLICATION NUMBER: US/10/174, 581
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
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PRIOR APPLICATION NUMBER: 60/063564
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
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PRIOR APPLICATION NUMBER: 60/069870
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

;; PRIOR APPLICATION NUMBER: 60/078886
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;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079786
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/080107
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080333
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;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
;; PRIOR APPLICATION NUMBER: 60/081070
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;; PRIOR APPLICATION NUMBER: 60/081195
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081838
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082568
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;; PRIOR APPLICATION NUMBER: 60/082569
;; PRIOR FILING DATE: 1998-04-21
;; PRIOR APPLICATION NUMBER: 60/082704
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/082797
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083495
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;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
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;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
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;; PRIOR APPLICATION NUMBER: 60/084640
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
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;; PRIOR APPLICATION NUMBER: 60/086023
;; PRIOR FILING DATE: 1998-05-18
;; PRIOR APPLICATION NUMBER: 60/086392
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/086486
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087098
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087208
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087609

;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
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;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
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;; PRIOR FILING DATE: 1998-06-10
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;; PRIOR APPLICATION NUMBER: 60/088825
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;; PRIOR APPLICATION NUMBER: 60/088826
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;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088863
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089090
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAACGPAAGYCLLGLHLFLITAGPALGNDPDRMLIRDVKALTLYHRYTTSRRLLP 60
|||
Db 1 MAAACGPAAGYCLLGLHLFLITAGPALGNDPDRMLIRDVKALTLYHRYTTSRRLLP 60
|||
QY 61 IPQLKCVGAGTACDSTTPRVIOQNKGMGNYVQNECKTDLDIAYXFGTIVSCEGYESS 120
|||
Db 61 IPQLKCVGAGTACDSTTPRVIOQNKGMGNYVQNECKTDLDIAYXFGTIVSCEGYESS 120
|||
QY 121 EDPYVLRGSCGLEYNDYELGLQKLKESGKHGFASFDDYVYKMSADSCKMSGLITTV 180
|||

```

Db      121 EDQVLRGSGLEBYNDYTELGLOKLESKGQHGFPASPSDYVYKMSADSCKNSGLITIV 180
Qy      181 VLLGIATVYVKLFPSDQYSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240
        181 VLLGIATVYVKLFPSDQYSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240
Qy      241 GATSGFSAFTGQGGYENSQPGFWTGLGTGGLIGYLFSGNRAATPFSDSWYPSYPSYP 300
        241 GATSGFSAFTGQGGYENSQPGFWTGLGTGGLIGYLFSGNRAATPFSDSWYPSYPSYP 300
Db      241 GATSGFSAFTGQGGYENSQPGFWTGLGTGGLIGYLFSGNRAATPFSDSWYPSYPSYP 300
Qy      301 GTWNRAYSPLHGSGGSYSVCSNSDTKTRTASGYGTRRR 339
        301 GTWNRAYSPLHGSGGSYSVCSNSDTKTRTASGYGTRRR 339

```

```

RESULT 11
US-10-176-483-504
; Sequence 504, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C68
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 504
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-483-504

```

```

Query Match      100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDVYKALTLHYDRYTTSRRLDP 60
        1 MAAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDVYKALTLHYDRYTTSRRLDP 60
Db      1 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAYKFGKTVSCGEYESS 120
        61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAYKFGKTVSCGEYESS 120
        61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAYKFGKTVSCGEYESS 120
Qy      121 EDQVLRGSGLEBYNDYTELGLOKLESKGQHGFPASPSDYVYKMSADSCKNSGLITIV 180
        121 EDQVLRGSGLEBYNDYTELGLOKLESKGQHGFPASPSDYVYKMSADSCKNSGLITIV 180
        121 EDQVLRGSGLEBYNDYTELGLOKLESKGQHGFPASPSDYVYKMSADSCKNSGLITIV 180
Db      121 EDQVLRGSGLEBYNDYTELGLOKLESKGQHGFPASPSDYVYKMSADSCKNSGLITIV 180
Qy      181 VLLGIATVYVKLFPSDQYSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240
        181 VLLGIATVYVKLFPSDQYSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240
        181 VLLGIATVYVKLFPSDQYSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240
Db      241 GATSGFSAFTGQGGYENSQPGFWTGLGTGGLIGYLFSGNRAATPFSDSWYPSYPSYP 300
        241 GATSGFSAFTGQGGYENSQPGFWTGLGTGGLIGYLFSGNRAATPFSDSWYPSYPSYP 300
Qy      301 GTWNRAYSPLHGSGGSYSVCSNSDTKTRTASGYGTRRR 339
        301 GTWNRAYSPLHGSGGSYSVCSNSDTKTRTASGYGTRRR 339
        301 GTWNRAYSPLHGSGGSYSVCSNSDTKTRTASGYGTRRR 339

```

```

RESULT 12
US-10-176-749-504
; Sequence 504, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 504
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-504

```

```

Query Match      100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDVYKALTLHYDRYTTSRRLDP 60
        1 MAAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDVYKALTLHYDRYTTSRRLDP 60
Db      1 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAYKFGKTVSCGEYESS 120
        61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAYKFGKTVSCGEYESS 120
        61 IPOLKCVGTAGCDSTTPKVIQCONKGMGVDYVQMECKTDLDIAYKFGKTVSCGEYESS 120
Qy      121 EDQVLRGSGLEBYNDYTELGLOKLESKGQHGFPASPSDYVYKMSADSCKNSGLITIV 180
        121 EDQVLRGSGLEBYNDYTELGLOKLESKGQHGFPASPSDYVYKMSADSCKNSGLITIV 180
        121 EDQVLRGSGLEBYNDYTELGLOKLESKGQHGFPASPSDYVYKMSADSCKNSGLITIV 180
Db      121 EDQVLRGSGLEBYNDYTELGLOKLESKGQHGFPASPSDYVYKMSADSCKNSGLITIV 180
Qy      181 VLLGIATVYVKLFPSDQYSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240
        181 VLLGIATVYVKLFPSDQYSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240
        181 VLLGIATVYVKLFPSDQYSPPPYSEYPPSHRYQRTNSAGPPPGFKSEFTGPONTGH 240
Db      241 GATSGFSAFTGQGGYENSQPGFWTGLGTGGLIGYLFSGNRAATPFSDSWYPSYPSYP 300
        241 GATSGFSAFTGQGGYENSQPGFWTGLGTGGLIGYLFSGNRAATPFSDSWYPSYPSYP 300
Qy      301 GTWNRAYSPLHGSGGSYSVCSNSDTKTRTASGYGTRRR 339
        301 GTWNRAYSPLHGSGGSYSVCSNSDTKTRTASGYGTRRR 339
        301 GTWNRAYSPLHGSGGSYSVCSNSDTKTRTASGYGTRRR 339

```

```

RESULT 13
US-10-176-914-504
; Sequence 504, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

```

```
/ APPLICANT: Zhang,Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C83
/ CURRENT APPLICATION NUMBER: US/10/176,914
/ PRIOR APPLICATION DATE: 2002-06-20
/ PRIOR APPLICATION removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 504
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-914-504
```

```
Query Match          100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No.4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLLRDVKALTLHYDRYTSRRLLDP 60
DB 1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLLRDVKALTLHYDRYTSRRLLDP 60
QY 61 IPOLKCVGAGTCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
DB 61 IPOLKCVGAGTCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
QY 121 EDQYVLRGSCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGLITTV 180
DB 121 EDQYVLRGSCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGLITTV 180
QY 181 VLLGIAFVYVKLFISDQYSPPPYSEYPPFSHRYPFTNSAGPPPGFSEFTGPQNTGH 240
DB 181 VLLGIAFVYVKLFISDQYSPPPYSEYPPFSHRYPFTNSAGPPPGFSEFTGPQNTGH 240
QY 241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSP 300
DB 241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSP 300
QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
```

```
RESULT 14
US-10-176-915-504
/ Sequence 504, Application US/10176915
/ Publication No. US20030017544A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C110
/ CURRENT APPLICATION NUMBER: US/10/176,915
/ PRIOR APPLICATION removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 504
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-915-504
```

```
Query Match          100.0%; Score 1879; DB 14; Length 339;
```

```
Best Local Similarity 100.0%; Pred. No.4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLLRDVKALTLHYDRYTSRRLLDP 60
DB 1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLLRDVKALTLHYDRYTSRRLLDP 60
QY 61 IPOLKCVGAGTCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
DB 61 IPOLKCVGAGTCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
QY 121 EDQYVLRGSCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGLITTV 180
DB 121 EDQYVLRGSCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGLITTV 180
QY 181 VLLGIAFVYVKLFISDQYSPPPYSEYPPFSHRYPFTNSAGPPPGFSEFTGPQNTGH 240
DB 181 VLLGIAFVYVKLFISDQYSPPPYSEYPPFSHRYPFTNSAGPPPGFSEFTGPQNTGH 240
QY 241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSP 300
DB 241 GATSGFGSAFTGQOQYENSGPGFWTGLGTGILGYLFGSNRAATPFSDSWYTPSPSP 300
QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
```

```
RESULT 15
US-10-173-706-504
/ Sequence 504, Application US/10173706
/ Publication No. US20030022293A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C7
/ CURRENT APPLICATION NUMBER: US/10/173,706
/ PRIOR APPLICATION removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 504
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-173-706-504
```

```
Query Match          100.0%; Score 1879; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No.4e-165;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLLRDVKALTLHYDRYTSRRLLDP 60
DB 1 MAAACGPGAGYCLLIGLHLFLITAGPALGMDPDRMLLRDVKALTLHYDRYTSRRLLDP 60
QY 61 IPOLKCVGAGTCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
DB 61 IPOLKCVGAGTCDSTTPKVIQCONKGMGDYDVQWECKTDLDIAVYKFTVVSCEGYESS 120
QY 121 EDQYVLRGSCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGLITTV 180
DB 121 EDQYVLRGSCGLEYNLDYTELGLQKLKESGKHGFASFSDYYKMSADSCKMSGLITTV 180
```

Qy	181	VLLGIATVWVYKLFPLSDCOYSPPPYSEYPPFPHRYORFTNSAGPPPGPKSEFTGPONTGH	240
Db	181	VLLGIATVWVYKLFPLSDCOYSPPPYSEYPPFPHRYORFTNSAGPPPGPKSEFTGPONTGH	240
Qy	241	GATSGFGSAFTGQGGYENSGPGFWTGLGTGGIILGYLFGSNRAATPFSDSWYTPSYPPSY	300
Db	241	GATSGFGSAFTGQGGYENSGPGFWTGLGTGGIILGYLFGSNRAATPFSDSWYTPSYPPSY	300
Qy	301	GTWNRAYSPLHGGSGSYSCNSDPTKTRTASGYGTRRR	339
Db	301	GTWNRAYSPLHGGSGSYSCNSDPTKTRTASGYGTRRR	339

Search completed: July 14, 2005, 20:37:49
 Job time : 107.864 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 20:14:28 ; Search time 23.2757 Seconds

(without alignments)
1401.351 Million cell updates/sec

Title: US-10-019-151C-2

Perfect score: 1879
Sequence: 1 MAACGPGAGYCTLLGLHL.....CNSDPKTRRAGYGGTRR 339Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499.5	26.6	323	2 T24582	hypothetical prote
2	115	6.1	407	2 T21956	hypothetical prote
3	115	6.1	1400	2 T31555	hypothetical prote
4	113	6.0	2090	2 S26058	probable transform
5	108.5	5.8	528	2 G02127	fus-like protein -
6	107	5.7	532	2 S27372	beta-fructofuranos
7	106.5	5.7	748	2 T04011	hypothetical prote
8	106	5.6	455	1 T21089	acid phosphatase (
9	106	5.6	1585	2 T31611	hypothetical prote
10	105	5.6	3300	2 D70575	probable PP2 prote
11	104	5.5	353	2 B34504	heterogeneous nucl
12	103.5	5.5	373	2 S40777	heterogeneous ribo
13	102.5	5.5	342	2 T45886	RNA-binding protei
14	101.5	5.4	794	2 T10519	pre-pro-1egumlin -
15	101.5	5.4	1844	2 T51890	related to Nup98-N
16	100.5	5.3	186	2 S28021	rab18 protein - Ar
17	100.5	5.3	314	2 T08675	hypothetical prote
18	100.5	5.3	462	4 S33798	FUS/CHOP mutant fu
19	100.5	5.3	526	1 S33799	RNA-binding protei
20	100	5.3	615	2 T29550	hypothetical prote
21	99.5	5.3	365	2 A34840	heterogeneous ribo
22	99.5	5.3	419	2 T04886	DAG protein homolo
23	99	5.3	632	2 T02627	hypothetical prote
24	98.5	5.2	320	1 DDKT	helix-destabilizin
25	98.5	5.2	320	1 A44485	heterogeneous ribo
26	98.5	5.2	320	2 S04617	heterogeneous ribo
27	98	5.2	1436	2 B70520	probable PP2 prote
28	98	5.2	1567	2 S11672	ice nucleation pro
29	97.5	5.2	925	2 JC2033	G protein-coupled

30	96.5	5.1	320	2 S30192	heterogeneous ribo
31	96.5	5.1	320	2 S02061	heterogeneous ribo
32	96.5	5.1	404	2 B84745	probable RNA-bindi
33	96.5	5.1	925	2 T19361	hypothetical prote
34	96.5	5.1	1732	2 T43026	probable DNA-direc
35	96	5.1	159	2 C49773	ecdysone-dependent
36	95.5	5.1	334	2 S53490	RNA-binding protei
37	95.5	5.1	658	2 T08153	cysteine proteinas
38	95	5.1	532	2 S27373	beta-fructofuranos
39	95	5.1	671	2 A35912	homeotic protein o
40	95	5.1	1239	2 T13809	homeotic protein o
41	94.5	5.0	284	2 B41224	homeotic protein p
42	94.5	5.0	298	2 A40616	34K antigen - Myco
43	94.5	5.0	406	2 G71404	probable ribonucle
44	94.5	5.0	465	2 S33680	ribonucleoprotein
45	94.5	5.0	471	2 S33679	ribonucleoprotein

ALIGNMENTS

RESULT 1

T24582

hypothetical protein T06D8.9 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 09-Jul-2004

C/Accession: T24582

R/Palmer, S.

Submitted to the EMBL Data Library, April 1995

A/Reference number: Z19909

A/Accession: T24582

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-323 <WIL>

A/Cross-references: UNIPROT:Q22254; EMBL:Z49130; PIDN:CAA8972.1; GSPDB:GN00020; CESP:T

A/Experimental source: clone T06D8

C/Genetics:

A/Gene: CESP:T06D8.9

A/Map position: 2

A/Intons: 7/3; 33/1; 109/3; 239/2

Query Match	Score	26.6%	DB 2	Length	323;
Best Local Similarity	34.8%		Pred. No. 1.3e-11;		
Matches	120;	Conservative	40;	Mismatches	88;
				Indels	97;
				Gaps	9;
QY	35	DRMLADVYALTLHARDRTTSRLDIPQLKCVGTAGCDSTPKVIOQONKMGDGYDVQ	94		
DB	36	DKVTLADVSAITLHKIGKMTTGRVSPFPQLKCVGSAAK-GAIPKVVQCANQGFDSDVQ	94		
QY	95	WEGCTDDLDIAVYFKGKTIVSGEYSESDQVTLRSGCGLEYNLDYBL-GLQKLKESGKH	153		
DB	95	WRCDADLPDMDFGSISSCEGDVADPDYILRSGSGLEYELRYNSASGNRSVRSKSD	154		
QY	154	GFASFSDYYKWSADSCMSGLITIVLGAIFVYKFLPSDQ-----	198		
DB	155	RNDQFA-----TFVVAFAIYIYIAWNNQNPBSSGYTSGSGCP	196		
QY	199	-----YSPPYSEYPPFSHRVQRFNTSAGPPPPKSEFT---GPONTG	239		
DB	197	GGGSGGGGGGPGGYSAAPPYDDY-----SKPPYGRGDSGSGGCGSS	243		
QY	240	HGATSGFGSAFTGQCGQYENSQPGFTGLTGILGLYLPSS-----NRATPPSDSWYRPS	294		
DB	244	SGGASGSGA-----NNGGSFWTGAISLGAIGYTLASSPLNNNAVYARP-----	285		
QY	295	YPPSYPGTNRAYSPPLHGSGSYVCSNBDYTRTASGYGTRRR	339		
DB	286	-----RNRGPFQDTGRFSSDSMSSPSTSMRSSSGTGITRR	323		

RESULT 2

T21956

hypothetical protein F38B7.3 - Caenorhabditis elegans

Db 182 GCG 184

RESULT 6

S27372

beta-fructofuranosidase (EC 3.2.1.26) 1 precursor - yeast (Saccharomyces cerevisiae)

N/Alternate names: Invertase; saccharase

C/Species: Saccharomyces cerevisiae

C/Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 09-Jul-2004

C/Accession: S27372; 825441

R/Hohmann, S.
submitted to the EMBL Data Library, November 1988

A/Reference number: S27372

A/Accession: S27372

A/Molecule type: DNA

A/Residues: 1-532 <HOH>

A/Cross-references: UNIPROT:P10594; EMBL:X07570; NID:g4567; PID:CAA30457.1; PID:g4568

R/Hohmann, S.; Gozalbo, D.

Mol. Gen. Genet. 211, 446-454, 1988

A/Title: Structural analysis of the 5' regions of yeast SUC genes revealed analogous pal

A/Reference number: S25439; MUID:88216256; PMID:2835632

A/Accession: S25441

A/Molecule type: DNA

A/Residues: 1-74 <HO2>

A/Cross-references: EMBL:X07570

C/Genetic81

A/Gene: SUC1

A/Map position: 7R

C/Superfamily: beta-fructofuranosidase

C/Keywords: glycosidase; hydrolase

F/1-19/Domain: signal sequence #status predicted <STG>

F/20-532/Product: beta-fructofuranosidase 1 #status predicted <MT>

Query Match

Best Local Similarity 5.7%; Score 107; DB 2; Length 532;

Matches 92; Conservative 40; Mismatches 144; Indels 106; Gaps 24;

QY 14 LLLGLHFLTAG-----PALGW-NDPRLMLRDVRLTLH-Y 49

DB 1 MLLQAFPLFL-AGFAKISAMTNETSDRLVHFTPKGWMNDNG-LWYDAKKGXWMLY 58

QY 50 DRYTTSRLDPIPOLKCVGAGCDSTY-----PKVIQCQKMGDGYDVQMECTDIDIA 104

DB 59 FQTNPN- -DTWGLPLFWGHANSDDLTHMODEFVALPAKKKSGAY-----SGSNVID 109

QY 105 YK-----FGKTV-----VSCGEYS--SBDQVYLRGSCGLEYNLD--YTETGLQK--L 146

DB 110 YNNTSGFFNDTIDPRQCVAILMTNTPESBEQY-----SYLDDGYFTETQKRPVL 162

QY 147 KESGKHGFASPSDYT---KSSADSCKMSGLITTVLGI-AFVVYKLFISDG--- 197

DB 163 AASTQ--FRDPKFWYBPSKMMIMTAKSQDYKIEIYSSDDLKSMLESFANEGFLGY 220

QY 198 QYSP-----PYSEYPPFSHRVQKFTNSAGBPPRG-FKSEFTGPGQNTGH-----GATS 244

DB 221 QYBCEGLIYVPSBDEPKSHVMFISINPGAPAGSGSNQYFVSGFNHGFBAFDNQRV 280

QY 245 GFGSAPFGQGYENSGPFTGTGLTGILGFLFGSNRAATPFPSWYTPSPSPYSGTN 304

DB 281 DFGMDYVALQTFPTDPT-----GSALGIAMASN-----WYSAPVPSNP--WR 323

QY 305 RAYSPLHGGSGSYVCSNDDTK 326

DB 324 SSMSLVAPFSLINTEYQANPETE 345

RESULT 7

T04011

hypothetical protein T5L19.200 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C/Accession: T04011

R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, March 1999

A/Reference number: Z15184

A/Accession: T04011

A/Molecule type: DNA

A/Residues: 1-748 <BEV>

A/Cross-references: UNIPROT:Q9T0G5; EMBL:AL049481

A/Experimental source: cultivar Columbia; BAC clone T5L19

C/Genetics:

A/Map position: 4

A/Introns: 67/2; 209/3; 271/3; 305/3; 329/3; 367/3; 691/1

A/Note: T5L19.200

Query Match

Best Local Similarity 5.7%; Score 106.5; DB 2; Length 748;

Matches 41; Conservative 23; Mismatches 45; Indels 57; Gaps 10;

QY 195 SDGQSPPESEVP--PFSHRVQKFTNSAG-----PPPGPKB-----FTGPON 237

DB 396 SRGFHAHPYDHPRGYSQ-GSYNSPFGGYPPQAMPPRGYGTDMQRPYSGPN 454

QY 238 TGHGATSGFSAFTGQGYENSGP-----GFWTGLGTG---ILGYLFGSNRA-----A 283

DB 455 -----YXGRGASAGVPVPPSGVPSPAPGPPPLSGVSYGYGSGHGPYGA 502

QY 284 TPSPDSMY-----YPSYPPSGTMMRAYEPPLGGSSSY 317

DB 503 APYSQNGYQQTGYQTYEOPRYDSNPMQP-PYGGSYPPAGGQSGY 547

RESULT 8

T21089

acid phosphatase (EC 3.1.3.2) purple homolog F18E2.1, precursor [similarity] - Caenorh

N/Alternate names: purple acid phosphatase (PAP)

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T21089

R/Lighting, J.
submitted to the EMBL Data Library, June 1996

A/Reference number: Z19372

A/Accession: T21089

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1455 <RTL>

A/Cross-references: UNIPROT:Q19553; EMBL:Z75537; PID:CAA99834.1; GSPDB:GN00023; CESP:F

A/Experimental source: clone F18E2

C/Genetics:

A/Gene: CESP:F18E2.1

A/Map position: 5

A/Introns: 48/1; 96/1; 178/3; 255/3; 292/3; 337/3; 424/2

C/Superfamily: kidney bean purple acid phosphatase; phosphoesterase core homology

C/Keywords: glycoprotein; iron; metalloprotein; phosphoric monoester hydrolase; zinc

F/117-189/Domain: phosphoesterase core homology <PEC>

F/123,152,155,321/Binding site: iron (Asp, Asp, Tyr, His) #status predicted

F/130,194,388/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/187,272,319/Binding site: zinc or manganese (Asp, Asn, His, His) #status predicted

F/188/Active site: His #status predicted

Query Match

Best Local Similarity 5.6%; Score 106; DB 1; Length 455;

Matches 59; Conservative 33; Mismatches 96; Indels 82; Gaps 16;

QY 93 VQNECKTDLDAVKGFTVSCSG-YSSSDQYVLRG-----SGLEYNLDY--- 138

DB 40 VVNTTSEVSQDVTYGTSGATSTAKGSEAVFGITRYRKALIMTGLEYSTEDYTI 99

QY 139 --TELGIQKLKESGKHGFASPSDY--YKKSSASDC---NMSGILITVILGLAFVYVK 192

DB 100 ASRKPSFKTSLNDPQSTKVCVFDGLGWHGNSYTESIIKGLADPDFYVHG--DIAYDL 157

QY 193 FLSDGQSPPESEVPF-----SHR--YQFTNSAGPPPGFKSRTGPONTG 239

DB 158 HTNNGQVGSYLVAVFPLISKVPYVVIAGNHEDDYQNTN-----YQKRFSVDPN-G 208

QY 240 HGATSGFGSAFTGCGYF-NSGPGFWTGLGTGILGLF----- 277
Db 209 H-----NDNQRYSPDLGPFVHWGVST-ETVGYEYEGMDPVMTQYDMLKDLTTA 257
QY 278 GSNRAATPFSDSWYTP-SYPPSYPGTMNRA 306
Db 258 NSNRRAHP-----WITFGHRFPYCSNVNSA 283

RESULT 9
T31611
hypothetical protein Y50E8A.g - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C/Accession: T31611
R/Steward, C.
submitted to the EMBL Data Library, September 1999
A/Reference number: Z21047
A/Accession: T31611
A/Status: preliminary; translated from GB/EMBL/DDBI
A/Molecule type: DNA
A/Residues: 1-1585 <MIL>
A/Cross-references: EMBL:AL117200; NID:el549770; PIDN:CAB55050.1; CESP:Y50E8A.g
A/Experimental source: clone Y50E8A
C/Genetics:
A/Genes: CESP:Y50E8A.g
A/Introns: 25/3; 60/1, 133/2, 217/3, 270/3, 337/2, 400/1, 746/2

Query Match 5.6%; Score 106; DB 2; Length 1585;
Best Local Similarity 29.4%; Pred. No. 4.5;
Matches 42; Conservative 10; Mismatches 63; Indels 28; Gaps 5;

QY 195 SDGQYPPPYSEYRPPPSHRQFTNSAGPPPGFKSEFTGPONTGHGANSFGSARTGQ 254
Db 845 SCSGAAPP-----PP-----PPPPAPAPAPAPSSGSGSGSAAAGGCG 887
QY 255 GYENSQPGFWTGLGTGILGLFGSNRAATPFSDSWYTPSYPGTMNRAVSPHAG-G 313
Db 888 GSSGGYSGSGSSGSGSGSGSGSGSGSAPALP-----PPPPPPPPPPAPAPAPAP 940

QY 314 SGSYSVCSNDTKRTTASGYGT 336
Db 941 SGGYSGASGSGS---AAGGCGGS 960

RESULT 10
D70575
probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)
C/Species: *Mycobacterium tuberculosis*
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C/Accession: D70575
R/Cole, S.T.; Broesch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sultoni, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A/Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A/Reference number: A70500; MUID:9825987; PMID:9634220
A/Accession: D70575
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-3300 <COU>
A/Cross-references: GB:Z95324; GB:AL123456; NID:g3261760; PIDN:CAB08587.1; PID:el299834;
A/Experimental source: strain H37RV
C/Genetics:
A/Genes: PPE

Query Match 5.6%; Score 105; DB 2; Length 3300;
Best Local Similarity 38.0%; Pred. No. 13;
Matches 30; Conservative 8; Mismatches 15; Indels 26; Gaps 6;

QY 218 TNSAG-----PPPGFKSEFTGPQ---NTGHGATSGFGSAFTGCGYENSGPGFW 264

Db 2303 TSGAGPVVPLDIPAPFGNSTTSPSSGCFRNSGCGSSGCGNV-----GANN--GFW 2355
QY 265 ---TGLGTGILGLYFGS 279
Db 2356 NTFAGIDNSGLON--FGS 2372

RESULT 11
B34504
heterogeneous nuclear ribonucleoprotein B1 - human
N/Alternate names: heterogeneous ribonuclear particle protein B1; hnRNP protein B1; NEPH
N/Contents: heterogeneous nuclear ribonucleoprotein A2
C/Species: *Homo sapiens* (man)
C/Date: 22-Jun-1990 #sequence_revision 22-Jun-1999 #text_change 09-Jul-2004
C/Accession: A56845; B34504; A34504; S48057; PC2222; E61013; B56845
R/Kozu, T.; Heinrich, B.; Schaefer, K.P.
Genomics 25, 365-371, 1995
A/Title: Structure and expression of the gene (HNRPA2B1) encoding the human hnRNP protei
A/Reference number: A56845; MUID:95309902; PMID:7789969
A/Accession: A56845
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-353 <KOZ>
A/Cross-references: UNIPROT:P22626; GB:D28877; NID:g565642; PIDN:BA06031.1; PID:g565643
R/Burd, C.G.; Swanson, M.S.; Goelach, M.; Dreyfus, G.
Proc. Natl. Acad. Sci. U.S.A. 86, 9788-9792, 1989
A/Title: Primary structures of the heterogeneous nuclear ribonucleoprotein A2, B1, and
A/Reference number: A34504; MUID:9009350; PMID:2557628
A/Accession: B34504
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-353 <BUR>
A/Cross-references: GB:M29064; NID:g337452; PIDN:AAA60271.1; PID:g337453
A/Accession: A34504
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-2,15-353 <BU2>
A/Cross-references: GB:M29064
R/Biamonti, G.; Ruggiu, M.; Saccone, S.; della Valle, G.; Riva, S.
Nucleic Acids Res. 22, 1996-2002, 1994
A/Title: Two homologous genes, originated by duplication, encode the human hnRNP protei
A/Reference number: S48057; MUID:94301779; PMID:8029005
A/Accession: S48057
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-353 <BIA>
A/Cross-references: EMBL:U09122
R/Praad, S.; Walent, J.; Dittschilo, A.
Biochem. Biophys. Res. Commun. 204, 772-779, 1994
A/Title: ADP-ribosylation of heterogeneous ribonucleoproteins in HeLa cells.
A/Reference number: PC2221; MUID:95071393; PMID:7980541
A/Accession: PC2222
A/Molecule type: protein
A/Residues: 'XXX', 83-86, 'X', 88-93, 'X', 95-100 <PRA>
A/Experimental source: HeLa cells
A/Note: this protein was shown to be ADP-ribosylated
R/Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Geeser, B.;
Electrophoresis 11, 528-536, 1990
A/Title: Two-dimensional gel electrophoresis, protein electrophoresis and microsequenci
A/Reference number: A61002; MUID:91031404; PMID:1699755
A/Accession: E61013
A/Molecule type: protein
A/Residues: 63-69; 204-212, 214-220, 'F', 221-228 <BAU>
C/Genetics:
A/Genes: GDB:HNRPA2B1
A/Cross-references: GDB:377778; OMIM:600124
A/Map position: 7p15-7p15
A/Introns: 2/3; 14/3; 51/3; 100/3; 171/1; 205/1; 232/1; 253/1; 293/1; 334/1
C/Superfamily: helix-coil stabilizing protein; ribonucleoprotein repeat homology
C/Keywords: alternative splicing; duplication; nucleic acid binding
F/1-2,15-353/Domain: heterogeneous ribonuclear particle protein A2 <HA2>
F/22-88/Domain: ribonucleoprotein repeat homology <RHM1>

QY 311 HGGSGSYVCSNSDTRKRTA--SGYGGTR 337
 DB 425 GGGSGSYPGGGGIEGDTGTGTFPGSGGSR 453

RESULT 15

TS1890
 related to Nup98-Nup96 precursor [imported] - Neurospora crassa
 N/Alternate names: Protein B23111.20
 C/Species: Neurospora crassa
 C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
 C/Accession: TS1890
 R/Schulte, U.; Aign, V.; Hehlsel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, August 2000
 A/Reference number: Z25858
 A/Accession: TS1890
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1844 <SCH>
 A/Cross-references: EMBL:AL391572; GSPDB:GN00116; NCSP:B23111.20
 A/Experimental source: BAC clone B23111; strain OR74A
 C/Genetics:
 A/Gene: NCSP:B23111.20
 A/Map position: 6
 A/Introns: 34/1; 1281/3

Query Match 5.4%; Score 101; DB 2; Length 1844;
 Best Local Similarity 35.0%; Pred. No. 13;

Matches 48; Conservative 8; Mismatches 51; Indels 30; Gaps 9;

QY 215 QRFNAGAPPPPGFKSEFTGPONTGHG-ATSGFGS-AFTGQGG-----YENSGPGFW 264
 DB 11 QNTNTSGGFGSSGFCIN-TCTTGTCGAAITGCGAPAQITTTGGGFGSGTTGTTGGFG 69
 QY 265 T---GLGTGILGY--LFGSNRAATPFSDSWYTPSYPPSPGTWNRAYSPLHGSGSYS 318
 DB 70 TWTAGGFGTCGGGGAKPAGFSTPATY---GGGLFGSSTATATGT-----GGFGSTG 117
 QY 319 VCSNSDTRKRTASGYCG 335
 DB 118 FGSNTAT-TGTGFGSGG 133

Search completed: July 14, 2005, 20:33:16
 Job time : 31.2757 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:55:46 ; Search time 106.243 Seconds
(without alignments)
1633.949 Million cell updates/sec

Title: US-10-019-151C-2

Sequence: 1 MAAACGGAAAGYCLLLGLHL.....CSNSDTRTRRASGYGTRRR 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_tramb1:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1879	100.0	339	2	Q96BY9
2	1867	99.4	339	2	Q96BY9
3	1676	89.2	303	2	Q9UN23
4	1428	76.0	363	2	Q8R300
5	1427	75.9	334	2	Q8C6G7
6	1427	75.9	363	2	Q8D8R1
7	1418	75.5	363	2	Q8R2J3
8	1387	73.8	334	2	Q6A1X2
9	1176.5	62.6	292	2	Q8C2P1
10	499.5	26.6	323	2	Q222S4
11	361.5	19.2	357	2	Q7S303
12	124	6.6	965	2	Q7RW88
13	124	6.6	965	2	Q01385
14	124	6.6	977	2	Q8X005
15	122	6.5	974	2	Q9UVJ3
16	121.5	6.5	421	2	Q6Z8B6
17	121	6.4	587	2	Q98SL7
18	117	6.2	954	2	Q6C1L8
19	116.5	6.2	963	2	Q9UVI2
20	115	6.1	407	2	Q201S1
21	115	6.0	942	2	Q9W4N4
22	113.5	6.0	555	2	Q62D57
23	113	6.0	410	2	Q7ZUR3
24	113	6.0	2090	1	N214 HUMAN
25	113	6.0	2091	1	Q7SRF7
26	113	6.0	2119	2	Q86XJ3
27	112.5	6.0	197	2	Q9ATK3
28	112.5	6.0	366	2	Q8WYF8
29	112	6.0	1519	2	Q7Z3C4
30	111	5.9	571	2	Q7UR98
31	111	5.9	2850	1	HORN_HUMAN

32	110.5	5.9	592	2	Q98SL6	Q98SL6 xenopus lae
33	110.5	5.9	2058	2	Q7PUR9	Q7PUR9 anopheles g
34	110	5.9	350	2	Q8C2H8	Q8C2H8 mus musculus
35	110	5.9	898	2	Q8K588	Q8K588 mus musculus
36	110	5.9	911	1	ILP3 MOUSE	Q921X4 mus musculus
37	110	5.9	37	2	Q812A1	Q812A1 mus musculus
38	109.5	5.8	399	2	Q7ZXJ3	Q7ZXJ3 xenopus lae
39	109	5.8	410	2	Q16988	Q16988 araneus dia
40	109	5.8	633	2	Q86AP6	Q86AP6 dictyostell
41	108.5	5.8	528	2	Q13344	Q13344 homo sapien
42	108	5.7	262	2	Q90X89	Q90X89 xenopus tro
43	107.5	5.7	360	2	Q9LK74	Q9LK74 arabidopsis
44	107.5	5.7	365	2	Q6IP29	Q6IP29 xenopus lae
45	107.5	5.7	489	2	Q6WNS8	Q6WNS8 fugu rubrip

ALIGNMENTS

RESULT 1	ID	Q96BY9	PRELIMINARY;	PRT;	339 AA.
AC	Q96BY9				
DT	01-DEC-2001	(TrEMBLrel. 19, Created)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)			
DE	Hypothetical protein MG8721 (FOAP-7) (AAC1367).				
GN	Name=MG8721; Synonym=foap-7; ORFName=UNQ1967;				
OS	Homo sapiens (Human).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Uterus;				
RX	MBDILNB=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Halef F.,				
RA	Diatcienko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Shapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Ustin T.B., Tsohyunkil S., Carninci P., Prange C.,				
RA	Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mulhally S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,				
RA	Pathey J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,				
RT	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Uterus;				
RA	Strausberg R.J.				
RA	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Fujii Y., Teurttant K., Yajima Y., Amemiya T., Uka Y., Naito K.,				
RA	Kawaguchi A., Takayama K.;				
RA	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.				
RL	[4]				
RP	SEQUENCE FROM N.A.				
RX	MBDILNB=22887296; PubMed=12975309; DOI=10.1101/9r.1293003;				
RA	Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,				
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,				
RA	Baton D., Foster J., Grimaldi C., Gu O., Hase P.E., Heidens S.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				

RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh V., Smith V., Stinson J., Vages A.,
 RA Vanden R., Watanabe C., Wiedend D., Woods K., Xie M.H., Yantsu D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; BC015012; AAI15012.1; -;
 DR EMBL; AB028926; BAB82465.1; -;
 DR EMBL; AY359104; AAQ89462.1; -;
 DR InterPro; IPR009567; DUF1183.
 DR Pfam; PF06682; DUF1183; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 339 AA; 36975 MW; 83CC0517AB635FE9 CRC64;

Query Match 100.0%; Score 1879; DB 2; Length 339;
 Best Local Similarity 100.0%; Pred. No. 9e-135;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDVYKALTLHYDRYTSRRLD 60
 DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDVYKALTLHYDRYTSRRLD 60
 QY 61 IPOLKCVGTAGCDSTTPKVIQCONKMGVYVOMCKTDLIAVFKGTVCCEGYESS 120
 DB 61 IPOLKCVGTAGCDSTTPKVIQCONKMGVYVOMCKTDLIAVFKGTVCCEGYESS 120
 QY 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 DB 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 QY 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 DB 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 QY 181 VLLGIAFVYVKLFLSDQYSPPPYSRPPSHRYQFTNSAGPPPKSBEFTGPQNTGH 240
 DB 181 VLLGIAFVYVKLFLSDQYSPPPYSRPPSHRYQFTNSAGPPPKSBEFTGPQNTGH 240
 QY 241 GATSGGSAFTQCGGYSNPGPFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPSYP 300
 DB 241 GATSGGSAFTQCGGYSNPGPFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPSYP 300
 QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
 DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339

RESULT 2

QY683 PRELIMINARY; PRT; 339 AA.
 AC QY683;
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE HSPC035 protein (XTP3).
 GN Name=XTP3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
 RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
 RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,
 RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Liu Y., Cheng J., Lu Y., Wang G., Zhang L., Chen J., Li L.;
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF100748; AAD43012.1; -;
 DR EMBL; AF490252; AAO85460.1; -;
 DR InterPro; IPR009567; DUF1183.
 DR Pfam; PF06682; DUF1183; 1.
 SQ SEQUENCE 339 AA; 36979 MW; FB6FD94B3879FA8 CRC64;

Query Match 99.4%; Score 1867; DB 2; Length 339;
 Best Local Similarity 99.4%; Pred. No. 7.4e-134;
 Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDVYKALTLHYDRYTSRRLD 60
 DB 1 MAACGPGAGYCLLGLHLFLITAGPALGMDPDRMLRDVYKALTLHYDRYTSRRMD 60
 QY 61 IPOLKCVGTAGCDSTTPKVIQCONKMGVYVOMCKTDLIAVFKGTVCCEGYESS 120
 DB 61 IPOLKCVGTAGCDSTTPKVIQCONKMGVYVOMCKTDLIAVFKGTVCCEGYESS 120
 QY 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 DB 121 EDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGFASFSDYYKMSADSCKMSGLITIV 180
 QY 181 VLLGIAFVYVKLFLSDQYSPPPYSRPPSHRYQFTNSAGPPPKSBEFTGPQNTGH 240
 DB 181 VLLGIAFVYVKLFLSDQYSPPPYSRPPSHRYQFTNSAGPPPKSBEFTGPQNTGH 240
 QY 241 GATSGGSAFTQCGGYSNPGPFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPSYP 300
 DB 241 GATSGGSAFTQCGGYSNPGPFWTGLGTGILGYLFGSNRAATPPSDSWYPSYPSYP 300
 QY 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339
 DB 301 GTWNRAYSPLHGGSGSYVCSNSDTKTRTASGYGTRRR 339

RESULT 3

QYUN23 PRELIMINARY; PRT; 303 AA.
 AC QYUN23;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAY-2004 (T-EMBLrel. 26, Last annotation update)
 DE NP0003.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Normal pituitary;
 RA Huang Q., Zhou J., Song H., Peng J., Zhang Q., Fu G., Dai M., Mao Y.,
 RA Mao M., Chen Z., Chen J.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Normal pituitary;
 RA Hu R.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF078855; AAD44487.1; -;
 DR InterPro; IPR009567; DUF1183.
 DR Pfam; PF06682; DUF1183; 1.
 SQ SEQUENCE 303 AA; 33338 MW; 771609A6CF690F07 CRC64;

Query Match 89.2%; Score 1676; DB 2; Length 303;
 Best Local Similarity 99.7%; Pred. No. 2.2e-119;
 Matches 302; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 37 MLRDVYKALTLHYDRYTSRRMDPIPOLKCVGTAGCDSTTPKVIQCONKMGVYVOMCK 96
 DB 1 MLRDVYKALTLHYDRYTSRRMDPIPOLKCVGTAGCDSTTPKVIQCONKMGVYVOMCK 96
 QY 97 CKTDLIAVFKGTVCCEGYESSBDQYVLRSGCGLEYNLDYTELGLOKLKESGKHGF 156

Db 61 CKTDLDIAVKEKTVSCGEGYSSDDQVYLRGSCGLRYNLDYTELGQKLKESGKOHGA 120
 QY 157 SPSDYKWKMSADSCNMSGLTIVYLGIAFVYKFLPSDQYSPPPSEPPSHRQR 216
 Db 121 SPSDYKWKMSADSCNMSGLTIVYLGIAFVYKFLPSDQYSPPPSEPPSHRQR 180
 QY 217 FTNAGPFPKSEFTGPQNTGHTATSGPSAFTGQOYENSGPGFWTGTGTLGYL 276
 Db 181 FTNAGPFPKSEFTGPQNTGHTATSGPSAFTGQOYENSGPGFWTGTGTLGYL 240
 QY 277 FGSNRATPFSDSWYPSYPSYPTGTMNRAVSPLHGSGSYSCNSDTKTRTASGYGT 336
 Db 241 FGSNRATPFSDSWYPSYPSYPTGTMNRAVSPLHGSGSYSCNSDTKTRTASGYGT 300
 QY 337 RRR 339
 Db 301 RRR 303

RESULT 4
 Q8R300 PRELIMINARY; PRT; 363 AA.
 AC Q8R300; Q8N954;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE 1810045K07Rtk protein (Mus musculus cDNA file, clone TRACH2016709).
 DE Name=1810045K07Rtk;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Udén T.B., Toehlyuk S., Carninci P., Prange C., Raha S.S., Loguelfano N.A., Peters G.J., Adamson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Vallatton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzyzanski M.I., Skaleja U., Smallus D.E., Scherch A., Schein J.E., Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
 RA Strauberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3] SEQUENCE FROM N.A.
 RP Suzuki O., Sasaki N., Aotaka S., Shoji T., Ichihara T., Shiohara N., Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y., Matsumura Y., Moriya S., Chiba B., Momiyama H., Onogawa S., Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Katoka R., Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y., Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hito Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsumoto K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Magatsuna M., Murakawa K.,

RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahashi K., Masuo Y., Nagai K., Isega T.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC024888; AAH24888.1; -;
 DR EMBL; AK093942; BAB04255.1; -;
 DR MGD; MGI:1915137; 1810045K07Rtk.
 DR GO; GO:0016021; C:Integral to membrane; TAS.
 DR InterPro; IPR009567; DUF1183.
 DR Pfam; PF06682; DUF1183; 1.
 SQ SEQUENCE 363 AA; 38691 MW; 0457EA29DB6D3AB4 CRC64;
 Query Match 76.0%; Score 1428; DB 2; Length 363;
 Best Local Similarity 79.3%; Pred. No. 1,9e-100;
 Matches 268; Conservative 25; Mismatches 37; Indels 8; Gaps 4;
 QY 3 AACGPGAGYCLLGLHLLFLLTAGPALGMDPPMLRLDYKALTTHYDRYTSRRLLPIP 62
 Db 33 AAVGRPRAVRCPIILLLSLLLVAGPALGMDPPRLRLDYKALTLYSDRTSRRLLPIP 92
 QY 63 QLKCVGTAGCDSYTPRVIOCKNGMDYGVQVECTDLDIAVKEKTVSCGEGYSSD 122
 Db 93 QLKCVGTAGCDAVTPRVIOCKNGMDYGVQVECTDLDIAVKEKTVSCGEGYSSD 152
 QY 123 QYVLRGSCGLRYNLDYTELGQKLKESGKOHGAFSPDYKWKMSADSCNMSGLTIVYL 182
 Db 153 QYVLRGSCGLRYNLDYTELGQKLKESGKOHGAFSPDYKWKMSADSCNMSGLTIVYL 206
 QY 183 LGIAFVYKFLPSDQYSPPPSEPPSHRQRFTNAGPFPKSEFTGPQNTGHTATSG 242
 Db 207 FVIAFVYKFLPSDQYSPPPSEPPSHRQRFTNAGPFPKSEFTGPQNTGHTATSG 266
 QY 243 TSGFGSAFTGQOYENSGPGFWTGTGTLGYLFTGNSNRATPFSDSWYPSYPTG 302
 Db 267 TSGFGSAFTGQOYENSGPGFWTGTGTLGYLFTGNSNRATPFSDSWYPSYPTG 325
 QY 303 MN-RAYSPLHGSGSYSCNSDTKTRTASGYGTGTRR 339
 Db 326 MNSRAYSPLHGSGSYSCNSDTKTRTASGYGTGTRR 363

RESULT 5
 Q8C6G7 PRELIMINARY; PRT; 334 AA.
 AC Q8C6G7;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Mus musculus adult female placenta cDNA, RIKEN full-length enriched library, clone:1600026G18 product: similar to POAP-7.
 DE Name=1810045K07Rtk;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX [1] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Placenta;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Placenta;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3] SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Placenta;
 RA The PANTOM Consortium;
 RL the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RT Nature 420:563-573(2002).
RN [4]
RN RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Placenta;
RC MBDLINE=0049374; PubMed=11062159; DOI=10.1101/gr.145100
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komu H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RT Genome Res. 10:1617-1630(2000).
RN [5]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MBDLINE=005030913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoke S., Sasaki N., Carninci P.,
RA Komu H., Akiyama J., Niehi K., Kitsumai T., Taahiro H., Itoh M.,
RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara S., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RT Genome Res. 10:1757-1771(2000).
RN [6]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX Adachi T., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Furumishi Y., Furuo M.,
RA Hanagaki T., Hara A., Hayatsu N., Hizumoto K., Hirooka T., Hori F.,
RA Imocant K., Ishi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Komu H., Konda M., Koyasu S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai T.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamana K. I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK075744; BAC35924.1; -
DR MGD; MGI:1915137; 181004SK07rik.
DR GO; GO:0016021; C:integral to membrane; TMS.
DR InterPro; IPR009567; DUF1183.
DR Pfam; PF06682; DUF1183; 1.
SQ SEQUENCE 334 AA; 35856 MW; EA12FE138052BCC4 CRC64;

Query Match 75.9%; Score 1427; DB 2; Length 334;
Best Local Similarity 79.3%; Pred. No. 2,1e-100;
Matches 268; Conservative 25; Mismatches 37; Indels 8; Gaps 4;

QY 3 AACGPGAGCYLLGLHLFLTLTGAPLAKGNNDPPRMILRYKVALTLHYDRTTSSRLDPI 62
DB 4 AATGRRPALRCPLLILSLILVAGPLAKGNNDPRILRYKVALTLXSDYITTSRLDPI 63

QY QLKCVGTAGCDSYTPKVIQCNKGMWDGYDVOMECKTDDIAYKEGKTIVSCEGYESSED 122
DB 64 QLKCVGTAGCAEYTRVITGCGKMGWDGYDVOMECKTDDIAYKEGKTIVSCEGYESSED 123

QY 123 QYVLRGSGCLFNYLDYTELGLQKLKESGKHQHPASFSDDYTYWSSADSCNNSGLITIVL 182
DB 124 QYVLRGSGCLFNYLDYTELGLKKLKESGKHQG---FSDYHYKLVSDDSC---GPTITAVL 177

QY 183 LGIAFVYVYLFSLSDGQYSPRPYSEYRPFNRVORFTNSAGRPAPRKSEFTGPOMTGGA 242
DB 178 FVIAFVYVYLFSLSDGQSPRPYSEHYPYSEHSORFASAGAPRPKSEFTGPOMTGGA 237

QY 243 TSGFGSAPFTGQOQYENSGPGFTVGLTGGLTGGLTGFSNNAATPFSDDSYTPSPYRGT 302
DB 238 SSGFGSAPF---GCGQYSSGPGFMSGGLAGGLGLTGLTGSNNAATPFSDDSYTHRAYPPSHGGA 296

QY 303 WNVRAVSPPLHGGSGSYSCNSDPTKTRTASVGGGTERR 339

Db 297 WNSRAYSPLGGAGSTGCASSNADSRTRTASGTGTRR 334

RESULT 6

Q9DBR1 PRELIMINARY; PRT; 363 AA.

AC Q9DBR1; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810045K07 product:similar to F0AP-7 (1810045K07Rik protein).

DS Name=1810045K07Rik;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=1085660; PubMed=11217851; DOI=10.1036/35055500;

RA RIKEN PANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RA The PANTOM Consortium,

RT the RIKEN Genome Exploration Research Group Phase I & II Team;

RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=50499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama Y., Nishi K., Kitsuurai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K., Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hasegawa T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Saeki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tajima Y., Toya T., Yamamori T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RP [7]
 RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smaliv D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK007787; BAB25254.1; -
 DR EMBL; BC013497; AAH13497.1; -
 DR MGD; MGI:1915137; 1810045K07Rik.
 DR GO; GO:0016021; C:Integral to membrane; TMS.
 DR Interpro; IPR009567; DUF1183.
 DR Pfam; PF06682; DUF1183; 1.
 SQ SEQUENCE 363 AA; 38705 MW; 463BCB5E1080CF5 CRC64;

Query Match 75.9%; Score 1427; DB 2; Length 363;
 Best Local Similarity 79.3%; Pred. No. 2.3e-100;
 Matches 268; Conservative 25; Mismatches 37; Indels 8; Gaps 4;

QY 3 AACGPAAGYCLLGLHLFLTAGPALGWNDDPRMLRDVYKALTLYDRYTSRRLLPIP 62
 DB 33 AAVGRPALRCPLLLLSLLVAGPALGWNDDPRILRDVKALTYLSDRTTSRRLLPIP 92
 QY 63 QLCVGGTAGCDSYTPRVIOCKNGMDGYDVQWCKTDLDAIYKFGKTVVSCGYESSD 122
 DB 93 QLCVGGTAGCBAATPRVIOCKNGMDGYDVQWCKTDLDAIYKFGKTVVSCGYESSD 152
 QY 123 QYTLRGSCGLENYLDYTELGLQKLKESGKHGAFASPDYTYKSSADSCKMSGLITTVL 182
 DB 153 QYTLRGSCGLENYLDYTELGLKKLKESGKHG--FSDYYHKLYSSDSC--GPIITAVL 206
 QY 183 LGIAFVYVYKFLPSDQGYSPPEYSEYPPFSHRHYORFTNSAGPPPKFSEFTGPONTGGA 242
 DB 207 FVLAFAVYVYKFLPSDQGYSPPEYSEYSEHPSHRFASAGAPPPGKSEFTGPONTGGA 266
 QY 243 TSGFGSAFTGQOQGYENSGRPFMTGLGTGGLGLYLFSGNRAATPSPDSWYPPSPYPT 302
 DB 267 SSGFGSAF-GGQGYGSGRPFMTGLGTGGLGLYLFSGNRAATPSPDSWYPPSPYPT 325
 QY 303 WN-RAVYPLHGGSGSYVCSNSDPTKTRTASGYGCTRRR 339
 DB 326 WNSRAVYPLGGGAGSYVCSNSDPTKTRTASGYGCTRRR 363

RESULT 7

08R233
 ID 08R233 PRELIMINARY; PRT; 363 AA.
 AC 08R233;
 DT 01-JUN-2002 (TEMBUREL 21, Created)
 DT 01-JUN-2002 (TEMBUREL 21, Last sequence update)
 DT 01-MAR-2004 (TEMBUREL 26, Last annotation update)
 DE 1810045K07Rik protein.
 GN Name=1810045K07Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RX [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skaleka U., Smaliv D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022616; AAH22616.1; -
 DR MGD; MGI:1915137; 1810045K07Rik.
 DR GO; GO:0016021; C:Integral to membrane; TMS.
 DR Interpro; IPR009567; DUF1183.
 DR Pfam; PF06682; DUF1183; 1.
 SQ SEQUENCE 363 AA; 38747 MW; A99A614440A91EB4 CRC64;

Query Match 75.5%; Score 1418; DB 2; Length 363;
 Best Local Similarity 79.0%; Pred. No. 1.1e-99;
 Matches 267; Conservative 25; Mismatches 38; Indels 8; Gaps 4;

QY 3 AACGPAAGYCLLGLHLFLTAGPALGWNDDPRMLRDVYKALTLYDRYTSRRLLPIP 62
 DB 33 AAVGRPALRCPLLLLSLLVAGPALGWNDDPRILRDVKALTYLSDRTTSRRLLPIP 92
 QY 63 QLCVGGTAGCDSYTPRVIOCKNGMDGYDVQWCKTDLDAIYKFGKTVVSCGYESSD 122
 DB 93 QLCVGGTAGCBAATPRVIOCKNGMDGYDVQWCKTDLDAIYKFGKTVVSCGYESSD 152
 QY 123 QYTLRGSCGLENYLDYTELGLQKLKESGKHGAFASPDYTYKSSADSCKMSGLITTVL 182
 DB 153 QYTLRGSCGLENYLDYTELGLKKLKESGKHG--FSDYYHKLYSSDSC--GPIITAVL 206
 QY 183 LGIAFVYVYKFLPSDQGYSPPEYSEYPPFSHRHYORFTNSAGPPPKFSEFTGPONTGGA 242
 DB 207 FVLAFAVYVYKFLPSDQGYSPPEYSEYSEHPSHRFASAGAPPPGKSEFTGPONTGGA 266
 QY 243 TSGFGSAFTGQOQGYENSGRPFMTGLGTGGLGLYLFSGNRAATPSPDSWYPPSPYPT 302
 DB 267 SSGFGSAF-GGQGYGSGRPFMTGLGTGGLGLYLFSGNRAATPSPDSWYPPSPYPT 325
 QY 303 WN-RAVYPLHGGSGSYVCSNSDPTKTRTASGYGCTRRR 339

Db 326 WNSRAYSPGCGAGSYCASSNADSRRTTAGYGTGRRR 363

RESULT 8

Q6AYN2 PRELIMINARY; PRT; 334 AA.

AC O6AYN2; 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein MGC33866.
 GN Name=MGC33866;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN 1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton A., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,
 RA Kravitski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN 12)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Director MGC Project;
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC078979; AAH78979.1; -;
 DR InterPro: IPR009567; DUF1183.
 DR Pfam: PF06682; DUF1183; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 334 AA; 35885 MW; 6812CFBA8BD352DC CRC64;

Query Match 73.8%; Score 1387; DB 2; Length 334;
 Best Local Similarity 76.6%; Pred. No. 2.3e-97;
 Matches 259; Conservative 28; Mismatches 43; Indels 8; Gaps 4;

QY 3 AACGPGAAAGCCLLGLPLTLTGPRALGMDPRMLRDVKALTLHYDRYTSRRLLDPR 62
 Db 4 AAGRPRAVACLLLLSLFLLVAGPALCMKPNRILRLRDVALTLSDRTYTSRRLLDPR 63
 QY 63 QLKCVGGTAGCDSYTPRVVICQKMGDYQVQWQCKTDLDIAVKGFTVSCGYSSSED 122
 Db 64 QLKCVGGTAGCDAVTPRVVCCQKMGDYQVQWQCKTDLDIAVKGFTVSCGYSSSED 123
 QY 123 QYVLRSGCGLETVLDYTELGLQKLGKSGKQHGFPASFSDDYTKWSSADSCMSGLITTVL 182
 Db 124 QYVLRSGCGLETVLDYTELGLKLGKSGKQHGFPASFSDDYTKWSSADSCMSGLITTVL 177
 QY 183 LGIAFVYVYKFLSLSDGQYSPRYSEYRPFESHRYORFNTNSAGRRPRPKSRTGPNQNGKA 242
 Db 178 FVLAFFVYVYKFLSLSDGQYSPRYSEYRPFESHRYORFNTNSAGRRPRPKSRTGPNQNGKA 237
 QY 243 TSGFGSAFTGQCGYENSQGFMTGLGTGTLGYLFGSNRAATPFSDSWYYPSPYPGT 302

Db 238 SSGFGSAF-CGGSYASSGCFWISGLAGGLLYLFGSNRAATPFSDSWYHPSPSYACA 296

QY 303 WN-RAYSPHGGSGSYSCNSDTRTNAGYGTGRRR 339

Db 297 WNSHAYSPGCGAGGRYSASSNTESRRTTSGYGTGRRR 334

RESULT 9

Q8C2P1 PRELIMINARY; PRT; 292 AA.

AC Q8C2P1; 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
 length enriched library, clone:B430024120 product:similar to FOAP-7
 DE (fragment).
 GN Name=1810045K07R1k;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN 1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN 12)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN 13)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN 14)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN 15)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/9r.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachiaki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed capillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN 16)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Heshizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imocant K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno K., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL EMBL; AK088728; BAC40531.1; -
 DR MGD; MGI:1915137; 1810045K07Rlk.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR009567; DUF1183.
 DR Pfam; PF06682; DUF1183; 1.
 DR NON TER 1
 SQ SEQUENCE 292 AA; 31362 MW; 580900AEP9294C68 CRC64;

Query Match 63.6%; Score 1176.5; DB 2; Length 292;
 Best Local Similarity 79.9%; Pred. No. 26-81;
 Matches 223; Conservative 18; Mismatches 31; Indels 7; Gaps 3;

QY 3 AACGPGAGYCLLGLFLPLTAGPALGMNDPDRMLRDYKALTLHYDRYTSRLDPIR 62
 DB 21 AAGRPAAVACPILLLSLLLVAGPALGMNDPDRILRDYKALTLVDRYTSRLDPIR 80
 QY 63 QLKCVGGTAGCDSTYPRVIOCONKMGDYDQWCKTDLDAVYKGTIVVSCGYSSSD 122
 DB 81 QLKCVGGTAGCBAATPRVIOCONKMGDYDQWCKTDLDAVYKGTIVVSCGYSSSD 140
 QY 123 QYVLRGSCGLBYNDYELGLQKESGKHGFPSPSDYKYKSSADSCNMSGILITVVL 162
 DB 141 QYVLRGSCGLBYNDYELGLQKESGKHGFPSPSDYKYKSSADSCNMSGILITVVL 194
 QY 183 LGIAFVYVYKFLPLSDGQYSPPESEYPPSHRYQFTNSAGPPPGFSEFTGONTGCA 242
 DB 195 FVLAFAVYKFLPLSDGQSPPESEYPPSHRYQFTNSAGPPPGFSEFTGONTGCA 254
 QY 243 TSGFPGSAFTGQCGYENSQPGFMTGLGTGILGLYFGSNR 281
 DB 255 SSGFGSNAF-CGGQYSSGSGPGFMTGLGTGILGLYFGSNR 292

RESULT 10
 Q22254 PRELIMINARY; PRT; 323 AA.
 AC Q22254;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein T06D8.9.
 GN ORFName=T06D8.9;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peleoderinae; Caenorhabditis.
 OC NCB1_TaxID=6239;
 OX 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Submitter S.;
 RL EMBL; 249130; CAA88972.1; -
 DR PIR; T24582; T24582.
 DR WormBase; WBGene00011529; T06D8.9.
 DR WormPep; T06D8.9; CE02330.

DR InterPro; IPR009567; DUF1183.
 DR Pfam; PF06682; DUF1183; 1.
 DR KW Hypothetical protein.
 SQ SEQUENCE 323 AA; 34010 MW; 718BF6B22FE2D084 CRC64;

Query Match 26.6%; Score 499.5; DB 2; Length 323;
 Best Local Similarity 34.8%; Pred. No. 6-6e-30;
 Matches 120; Conservative 40; Mismatches 88; Indels 97; Gaps 9;

QY 35 DRMLRDYKALTLHYDRYTSRLDPIQLKCVGTAGCDSTYPRVIOCONKMGDYDQ 94
 DB 36 DKVLADVASITLHKQMTTGRVSPFLQKCVGSAGK-GAPFVKVQCANGQFDSVDQ 94
 QY 95 WCKTDLDAVYKGTIVVSCGYSSSDQYVLRGSCGLBYNDYELGLQKESGKHG 153
 DB 95 WRCADLPHDMEFGSIVSCEGYDYVLRGSCGLBYNDYELGLQKESGKHG 154
 QY 154 GFASPSDYKYKSSADSCNMSGILITVVLGLIAFVYVYKFLPLSDGQ----- 198
 DB 155 RWDQFA-----TPVVAFLIYIYAMWTRNQNPPSSGTYSGSGCP 196
 QY 199 -----YSPPESEYPPSHRYQFTNSAGPPPGFSEFT--GPONTG 239
 DB 197 GPGSGSGGGGPGGYSPAPPDYD-----SKPPEYGRGDSQSGGCGSS 243
 QY 240 HGATSGFSAFTGQCGYENSQPGFMTGLGTGILGLYFGS-----NRATPFSDSMTYPS 294
 DB 244 SGGASGSA-----NNGSFWTGAISLIGLYLASFLNNNAVYRP----- 285
 QY 295 YPSPYPGTWNRAVPLHGGSGSYVCSNPDYKRTAGYGGTTRR 339
 DB 286 -----RYNRGFPDPTGFSSDSSPSSTSMRSSSGIGGTTTR 323

RESULT 11
 Q7S303 PRELIMINARY; PRT; 357 AA.
 AC Q7S303;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=NCU07545.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCB1_TaxID=5141;
 OX 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Puccell S., Rehman B.,
 RA Bkine T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gierre S.,
 RA Kamal M., Kamysseilis M., Mauceli B., Bielke C., Rudd S., Fishman D.,
 RA Kystofowa S., Raamsen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
 RA Desouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
 RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbold D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
 Nature 0:0-0 (2003).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AABX0100415; EAA29822.1; -
 DR InterPro; IPR009567; DUF1183.
 DR Pfam; PF06682; DUF1183; 1.
 KW Hypothetical protein.

SEQUENCE 357 AA; 37217 MW; ES5B1FA5F276775 CRC64;

Query Match 19.2%; Score 361.5; DB 2; Length 357;

Best Local Similarity 31.8%; Pred. No. 2.3e-19; Mismatches 131; Indels 53; Gaps 14;

Matches 107; Conservative 46; Mismatches 131; Indels 53; Gaps 14;

35 DRMLDVALTLHYRDTTSLRLDPIPOLKCVGAGCDSTYPRK--IQCNKG--WDG 90

42 DAVLSINRSLTLTPNSKTTGRRLPIPOLKCTSSRTCLALASPHISLMRCVNGPRYDK 101

91 YDVQFCKT-DLDIAKFKGKTVSCGYSSESDQYLYRSGCLFNLDYTELGLQKLR- 148

102 EDIQWCTVPSLPTTLQSLSTVDYICGYPEDDYLYKSCGVEXYTLATEBERRRKYGHG 161

149 SGKQHFASF--SDYYKMSADSQMSGLITIVLLGI-APVYKFLFSDGQYPPY 204

162 NQNGNNGWMBEBSBNK-----AGYLFGLVFGVLGIVISACVQAG-----GV 208

205 SEYPPSHRYQRTNSAG-----PPPGFKSBFTGPONTGATSGPSAFT 251

209 NNGVPGAEGQRGMGGGGGGCGGCGGDMNDPPF-----YPSNGYGNKPSGSGQGS 261

252 GQGGYNSG--PQFTGLTGILGILYFGSNRAATPSPS---WYPSYPPSYPGTMMR 305

262 GQGGYNSG--PQFTGLTGILGILYFGSNRAATPSPS---WYPSYPPSYPGTMMR 305

306 AVSPLHGSGSYVCSN---SDTKRTASGSGTTRR 339

322 SWGS-SSSSRSTSGGNGSSGTTTSTGSGTSHR 357

RESULT 12

07RM88 PRELIMINARY; PRT; 961 AA.

AC 07RM88; 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

GN Name=NC03493.1;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;

RT [1]

RP SEQUENCE FROM N.A.

RC STRAIN=OR74A;

RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehan B.,

RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,

RA Seltreitoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

RA Roy A., Foley K., Naylor J., Thoman N., Barrett K., Gierke S.,

RA Kamal M., Kamysseus M., Mauceli B., Bielke C., Rudd S., Fishman D.,

RA Krysotova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,

RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmant S.A.,

RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freltag M.,

RA Paulsen I., Sachs M.S., Lander B.S., Nussba D.C., Birtag M.,

RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."

RT Nature 0:0-0(2003).

CC -! CAUTION: The sequence shown here is derived from an

CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL: AABX0100786; EAA26644.1; -.

DR InterPro: IPR010816; Het-C.

DR Pfam: PF07217; Het-C; 1.

KW Hypothetical protein

SQ SEQUENCE 961 AA; 102083 MW; 9656BD5377A9640B CRC64;

Query Match 6.6%; Score 124; DB 2; Length 961;

Best Local Similarity 22.4%; Pred. No. 0.76; Mismatches 65; Conservative 38; Mismatches 99; Indels 88; Gaps 14;

93 VQWECKTDLIAKFKGKTVSCGYSSESDQYLYRG-----SGGLE----- 133

572 VQWSRETHHDY-----KTLASSEYKEGHN-HVLANGQPMDRPGGHTSCGADGKHVA 625

134 -----YNDYTEL-----GLQKESGKHQFASFSDYYKMSADSQMSGLITI 179

626 GSLMKGIRDLDTAPSGGVGGGRPSSTGHKTYGSASSHHRVPTTGEAASY----- 679

180 VVLGLIAFVYVYKTLFSDQYSPPYSEY---PPFSHRVQRTNSAGPPPGFKSEFTGPQ 236

680 -----FSSADPRHASPPTDRYGRSPSSGYSVHGSGRSPAPAS--FGYH 725

237 NTGKATGFGSGLFTGQGY-ENGSPGWTGILGTGILYFGSNRAATPSPSY----- 291

726 HGHQAYRGSSTSSPSGSGPSY-----GSSGSPSYG-----PSQPSYSGQP 773

292 ----YPSY--PPSYPTWNRASPLHGSGSYVCSNDDTKRTASGYGG 335

774 SYSSQPSYGAPPSQPPYSGQ---PHYGAPHSYSGGRPPPPRPSGYG 820

RESULT 13

001385 PRELIMINARY; PRT; 966 AA.

AC 001385; 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

GN Name=het-COR.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;

RT [1]

RP SEQUENCE FROM N.A.

RC STRAIN=74-OR23-1VA;

RA Saue S.J., Kuldau G.A., Smith M.L., Glass N.L.;

RA Subtilted (Apr-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL: L77234; AAB48349.1; -

DR InterPro: IPR008277; 6DGDH_C-like.

DR pfam: PF07217; Het-C; 1.

RT signal.

FT NON TER

FT SIGNAL

SQ SEQUENCE 966 AA; 102790 MW; ADA9BD506222D202 CRC64;

Query Match 6.6%; Score 124; DB 2; Length 966;

Best Local Similarity 22.4%; Pred. No. 0.76; Mismatches 65; Conservative 38; Mismatches 99; Indels 88; Gaps 14;

93 VQWECKTDLIAKFKGKTVSCGYSSESDQYLYRG-----SGGLE----- 133

577 VQWSRETHHDY-----KTLASSEYKEGHN-HVLANGQPMDRPGGHTSCADGKHVA 630

134 -----YNDYTEL-----GLQKESGKHQFASFSDYYKMSADSQMSGLITI 179

631 GSLMKGIRDLDTAPSGGVGGGRPSSTGHKTYGSASSHHRVPTTGEAASY----- 684

180 VVLGLIAFVYVYKTLFSDQYSPPYSEY---PPFSHRVQRTNSAGPPPGFKSEFTGPQ 236

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:54:41 ; Search time 76.9612 Seconds

(without alignments)
1196.043 Million cell updates/sec

Title: US-10-019-151C-1

Sequence: 1 MILLVILAFILKQVDMLESI.....AGCCMGKQKQVMEGRGAS 238

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1243	100.0	238	4 AAB20089	Aab20089 Human hyd
2	1178	94.8	638	ADQ96030	Adq96030 T cell ac
3	1178	94.8	638	ADQ96032	Adq96032 T cell ac
4	1178	94.8	1070	6 ADA55285	Ada55285 Human pro
5	1178	94.8	1096	3 AAB43253	Aab43253 Human ORF
6	1178	94.8	1553	8 ADQ96036	Adq96036 T cell ac
7	1178	94.8	1726	2 AAY02377	Aay02377 Polypepti
8	1178	94.8	2141	5 ABB81196	Abb81196 Human PNI
9	1178	94.8	2376	6 ABR58313	AbR58313 BC0586 P
10	1178	94.8	2376	8 ADQ96034	Adq96034 T cell ac
11	983	79.1	1167	8 ADQ08792	AdQ08792 Ciona int
12	982	79.0	354	4 ABG04093	AbG04093 Novel hum
13	951	76.5	873	4 AAM93552	Aam93552 Human pol
14	951	76.5	873	8 ADL31282	AdL31282 Human pro
15	873	70.2	1766	4 ABB58631	AbB58631 Drosophila
16	653	52.5	2500	8 ADN23107	Adn23107 Bacterial
17	603	48.5	316	6 ABR52630	AbR52630 Protein c
18	603	48.5	316	7 ADK64762	AdK64762 Disease t
19	603	48.5	316	8 ADN06059	Adn06059 Antiporci
20	601.5	48.4	1248	4 ABG19706	AbG19706 Novel hum
21	581.5	46.8	178	6 ABO01269	AbO01269 Growth de
22	459	36.9	89	4 ABG02994	AbG02994 Novel hum
23	356.5	28.7	1283	8 ABB24334	AbB24334 Bacterial
24	352.5	28.4	1945	8 ADR66432	AdR66432 Aspergill
25	318.5	25.6	2016	8 ADP99054	Adp99054 C. albica

26	317	25.5	2100	8 ADN19489	Adn19489 Bacterial
27	270.5	21.8	328	4 ABG04094	Abg04094 Novel hum
28	256	20.6	1610	8 ADN20795	Adn20795 Bacterial
29	237	19.1	52	4 ABG19704	AbG19704 Novel hum
30	234	18.8	60	3 AAG02630	Ag02630 Human sec
31	231.5	18.6	2108	8 ADN18884	Adn18884 Bacterial
32	107.5	8.6	2000	6 ABR52606	AbR52606 Protein t
33	107.5	8.6	2000	6 ADK63610	AdK63610 Disease t
34	88.5	7.1	410	6 ABU33498	AbU33498 Protein e
35	87.5	7.0	4624	7 ADR78572	AdR78572 Dynein ax
36	87.5	7.0	4624	7 ADJ71185	AdJ71185 Human hea
37	86	6.9	252	6 ABM71071	Abm71071 Staphyloc
38	86	6.9	336	6 ABM70942	Abm70942 Staphyloc
39	86	6.9	414	6 ABU42356	Abu42356 Protein e
40	85.5	6.9	1318	8 ADL05937	AdL05937 M. catarr
41	85.5	6.9	2173	5 ABP69251	AbP69251 Human pol
42	85	6.8	217	4 ABG16902	AbG16902 Novel hum
43	84.5	6.8	679	7 ADM05878	Adm05878 Human pro
44	84.5	6.8	679	7 ADN39904	Adn39904 Cancer/an
45	84	6.8	806	3 AAY88055	AY88055 Murine To

ALIGNMENTS

RESULT 1
AAB20089 standard; protein; 238 AA.
ID AAB20089 ;

AC AAB20089 ;
XX
DT 23-APR-2001 (first entry)

XX Human hydrophobic domain-containing protein HP03303.

XX Human; hydrophobic domain; antiinflammatory; immunosuppressive;

XX immunostimulant; vulnerrary; antitumor; haemostatic; cytotoxic;

KW hepatotropic; thrombolytic; antitumor; antiviral; antibacterial;

KM antifungal; gene therapy; diagnosis; membrane protein.

XX Homo sapiens.

OS

XX

PH Key location/Qualifiers

FT Modified-site 29 /note= "N-glycosylated"

XX W0200100824-A2.

XX PD 04-JAN-2001.

XX PF 16-JUN-2000; 2000MO-JP003944.

XX PR 24-JUN-1999; 99JP-00178065.

XX (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

PA Kato S, Kimura T;

XX WPI; 2001-123008/13.

DR N-PSDB; AAB20089.

XX

PT New proteins with hydrophobic domains, useful for treating autoimmune

PS diseases, inflammatory diseases, wounds, burns, incisions and ulcers.

XX Claim 1; Page 85-86; 126pp; English.

CC The present sequence is that of a novel human protein having an N-

terminal transmembrane domain. It is predicted from cDNA clone HP03303

CC (see AAF00207), isolated from a human liver cDNA library. The predicted

CC protein shows sequence similarity to human hypotheoretical protein KIAA1007.

CC The invention provides human proteins (see AAB20089-96) having

CC hydrophobic domains indicative of secretory signals or membrane domains,

CC and nucleic acids (see AAF30020-27) encoding them. These are expected to
 CC have cell proliferation, cell differentiation, immunostimulant or
 CC immunosuppressor, haematopoiesis regulating, tissue growth, actinin,
 CC inhibin, chemotactic, chemokinetic, haemostatic, thrombolytic,
 CC receptor/ligand, antiinflammatory or antitumor activities (no evidence
 CC provided). Expression vectors, eukaryotic host cells and antibodies are
 CC also provided. The secreted or membrane proteins of the invention can be
 CC used as pharmaceuticals or antigens for preparing antibodies. Cells
 CC expressing them are utilized for detection of corresponding receptors or
 CC ligands, and in candidate drug screening

XX Sequence 238 AA;

Query Match 100.0%; Score 1243; DB 4; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.4e-131;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MILLVTLAFYLMQVDMSEINIAPRILTNFTGVMPQPKDLSYLTSPVTFLSDLRS 60
 |||||
 Db 1 MILLVTLAFYLMQVDMSEINIAPRILTNFTGVMPQPKDLSYLTSPVTFLSDLRS 60
 QY 61 NLOVSNBPGNRNVLQILNALVYVGTQALAHINKGSTPMSSTITSAHMDIFONTAVDL 120
 |||||
 Db 61 NLOVSNBPGNRNVLQILNALVYVGTQALAHINKGSTPMSSTITSAHMDIFONTAVDL 120
 QY 121 DTGGRYLFPLNAINOLRYPSNTHYFSCITMLYLPABANTBAIOEQITRVLLERLIYNRP 180
 |||||
 Db 121 DTGGRYLFPLNAINOLRYPSNTHYFSCITMLYLPABANTBAIOEQITRVLLERLIYNRP 180
 QY 181 PMGLITTFIEILINPAPKFWNHEFVHCAPRIEKLFGSVAQCCMGOKAQOVMESTGAS 238
 |||||
 Db 181 PMGLITTFIEILINPAPKFWNHEFVHCAPRIEKLFGSVAQCCMGOKAQOVMESTGAS 238

RESULT 2

ADQ96030 ID ADQ96030 standard; protein; 638 AA.

XX ADQ96030;

XX 07-OCT-2004 (first entry)

XX T cell activation associated protein #104.

XX antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV;
 KM antimicrobial; antirheumatic; immunosuppressive; neuroprotective;
 KM gene therapy; T cell activation; diagnosis; autoimmune disease;
 KM rheumatoid arthritis; asthma; multiple sclerosis; diabetes;
 KM allergic disease; infectious disease; AIDS; chronic rejection; organ;
 KM bone-marrow transplant.

XX Homo sapiens.

XX WO2004058805-A2.

XX 15-JUL-2004.

XX 25-DEC-2003; 2003WO-JP016715.

XX 26-DEC-2002; 2002JP-00376365.

XX 27-DEC-2002; 2002US-0436473P.

XX 25-APR-2003; 2003JP-00122113.

XX 28-APR-2003; 2003US-0465792P.

XX 21-OCT-2003; 2003JP-00360559.

XX 22-OCT-2003; 2003US-0512846P.

XX (ASAH-) ASAH KASEI PHARMA CORP.

XX Matsuuda A, Yoneta S;
 DR WPI, 2004-583134/57.
 DR N-PSDB; ADQ96029.
 XX

PT New purified protein involved in T cell activation, useful for
 PT diagnosis, preventing and/or treating acquired immunodeficiency
 PT syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic
 PT and infectious diseases.

XX Claim 1; SEQ ID NO 208; 2828pp; English.

XX The invention relates to purified proteins and genes encoding them, that
 CC are involved in T cell activation (I) and has an amino acid deletion,
 CC substitution or addition in the amino acid sequences. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of autoimmune disease (rheumatoid arthritis,
 CC asthma, multiple sclerosis and diabetes), allergic disease, infectious
 CC disease, AIDS, and acute or chronic rejection at organ transplant or bone
 CC marrow transplant. This sequence corresponds to a protein involved in T
 CC cell activation.

XX Sequence 638 AA;

Query Match 94.8%; Score 1178; DB 8; Length 638;
 Best Local Similarity 99.6%; Pred. No. 1.4e-123;
 Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMSEINIAPRILTNFTGVMPQPKDLSYLTSPVTFLSDLRSNLOVSNBPNRY 72
 :|||
 Db 413 KVDMLSEINIAPRILTNFTGVMPQPKDLSYLTSPVTFLSDLRSNLOVSNBPNRY 472
 QY 73 NQILNALVYVGTQALAHINKGSTPMSSTITSAHMDIFONTAVDLDTGERYFLN 132
 |||||
 Db 473 NQILNALVYVGTQALAHINKGSTPMSSTITSAHMDIFONTAVDLDTGERYFLN 132
 QY 133 ANOLRYPSNTHYFSCITMLYLPABANTBAIOEQITRVLLERLIYNRP 192
 |||||
 Db 533 ANOLRYPSNTHYFSCITMLYLPABANTBAIOEQITRVLLERLIYNRP 192
 QY 193 KNPAKFWNHEFVHCAPRIEKLFGSVAQCCMGOKAQOVMESTGAS 238
 |||||
 Db 593 KNPAKFWNHEFVHCAPRIEKLFGSVAQCCMGOKAQOVMESTGAS 638

RESULT 3

ADQ96032 ID ADQ96032 standard; protein; 638 AA.

XX ADQ96032;

XX 07-OCT-2004 (first entry)

XX T cell activation associated protein #105.

XX antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV;
 KM antimicrobial; antirheumatic; immunosuppressive; neuroprotective;
 KM gene therapy; T cell activation; diagnosis; autoimmune disease;
 KM rheumatoid arthritis; asthma; multiple sclerosis; diabetes;
 KM allergic disease; infectious disease; AIDS; chronic rejection; organ;
 KM bone-marrow transplant.

XX Homo sapiens.

XX WO2004058805-A2.

XX 15-JUL-2004.

XX 25-DEC-2003; 2003WO-JP016715.

XX 26-DEC-2002; 2002JP-00376365.

XX 27-DEC-2002; 2002US-0436473P.

XX 25-APR-2003; 2003JP-00122113.

XX 28-APR-2003; 2003US-0465792P.

XX 21-OCT-2003; 2003JP-00360559.
 XX 22-OCT-2003; 2003US-0512846P.
 XX (ASAH-) ASAH KASEI PHARMA CORP.

XX Matbuda A, Yoneta S;
 PI WPI, 2004-593134/57.
 DR N-PSDB; ADA96031.
 XX
 PT New purified protein involved in T cell activation, useful for
 PT diagnosing, preventing and/or treating acquired immunodeficiency
 PT syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic
 PT and infectious diseases.
 XX
 PS Claim 1; SEQ ID NO 210; 2828bp; English.
 XX
 CC The invention relates to purified proteins and genes encoding them, that
 CC are involved in T cell activation (T) and has an amino acid deletion,
 CC substitution or addition in the amino acid sequences. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of autoimmune disease (rheumatoid arthritis,
 CC asthma, multiple sclerosis and diabetes), allergic disease, infectious
 CC disease, AIDS, and acute or chronic rejection of organ transplant or bone
 CC marrow transplant. This sequence corresponds to a protein involved in T
 CC cell activation.
 CC
 XX
 SQ Sequence 638 AA;
 Query Match 94.8%; Score 1178; DB 8; Length 638;
 Best Local Similarity 99.6%; Pred. No. 1.4e-123;
 Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QVDMLESHINAPRLINFTGVMPPQPKDDSLKTRSPVTFSLDRSNQVSNENPNRY 72
 :|||||
 DB 413 KVDMLSEINAPRLINFTGVMPPQPKDDSLKTRSPVTFSLDRSNQVSNENPNRY 472
 QY 73 NLOLINALVLYVGTQAIHAIHNKSTPSMSTTHSAMDIFQNLAVDLDTREGRYLFLNAI 132
 :|||||
 DB 473 NLOLINALVLYVGTQAIHAIHNKSTPSMSTTHSAMDIFQNLAVDLDTREGRYLFLNAI 532
 QY 133 ANOLRYNSHTHYFSCMTLYLFAEANTBAIOEQITRVLERLIVNRHPWGLITITFELI 192
 :|||||
 DB 533 ANOLRYNSHTHYFSCMTLYLFAEANTBAIOEQITRVLERLIVNRHPWGLITITFELI 592
 QY 193 KNPAFKFMNHFVHCAPBEIKLFGSVAAQCCMGOKOAOQWEGTAS 238
 :|||||
 DB 593 KNPAFKFMNHFVHCAPBEIKLFGSVAAQCCMGOKOAOQWEGTAS 638
 RESULT 4
 ID ADA55285
 AC ADA55285 standard; protein; 1070 AA.
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human protein, SEQ ID 2853.
 XX
 KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
 KW Inflammatory disease; osteoporosis; neurological disease.
 XX
 OS Homo sapiens.
 XX
 PN EP1293569-A2.
 XX
 PD 19-MAR-2003.
 XX
 PF 21-MAR-2002; 2002EP-00006586.
 XX
 PR 14-SEP-2001; 2001JP-00328381.
 XX
 PR 24-JAN-2002; 2002US-0350435P.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Ieogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;
 XX
 DR WPI; 2003-395539/38.
 DR N-PSDB; ADA53646.
 XX
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.
 XX
 PS Claim 14; SEQ ID NO 2853; 2055bp; English.
 XX
 CC The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.
 CC
 XX
 SQ Sequence 1070 AA;
 Query Match 94.8%; Score 1178; DB 6; Length 1070;
 Best Local Similarity 99.6%; Pred. No. 3e-123;
 Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QVDMLESHINAPRLINFTGVMPPQPKDDSLKTRSPVTFSLDRSNQVSNENPNRY 72
 :|||||
 DB 845 KVDMLSEINAPRLINFTGVMPPQPKDDSLKTRSPVTFSLDRSNQVSNENPNRY 904
 QY 73 NLOLINALVLYVGTQAIHAIHNKSTPSMSTTHSAMDIFQNLAVDLDTREGRYLFLNAI 132
 :|||||
 DB 905 NLOLINALVLYVGTQAIHAIHNKSTPSMSTTHSAMDIFQNLAVDLDTREGRYLFLNAI 964
 QY 133 ANOLRYNSHTHYFSCMTLYLFAEANTBAIOEQITRVLERLIVNRHPWGLITITFELI 192
 :|||||
 DB 965 ANOLRYNSHTHYFSCMTLYLFAEANTBAIOEQITRVLERLIVNRHPWGLITITFELI 1024
 QY 193 KNPAFKFMNHFVHCAPBEIKLFGSVAAQCCMGOKOAOQWEGTAS 238
 :|||||
 DB 1025 KNPAFKFMNHFVHCAPBEIKLFGSVAAQCCMGOKOAOQWEGTAS 1070
 RESULT 5
 ID AAB43253
 AC AAB43253 standard; protein; 1096 AA.
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORF3017 polypeptide sequence SEQ ID NO:6034.
 XX
 KW Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
 KW Vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; anticytoid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 XX
 OS Homo sapiens.
 XX
 PN WO200058473-A2.
 XX
 PD 05-OCT-2000.

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XX 31-MAR-2000; 2000MO-US008621.
PF 31-MAR-1999; 99US-0127607P.
XX 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
XX 30-MAR-2000; 2000US-00540763.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinketsu RA, Leach M;
XX
XX WPI; 2000-602362/57.
XX
XX DR N-PSDB; AAC77462.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
XX useful for treating e.g. cancers, proliferative disorders,
XX neurodegenerative disorders and cardiovascular disease.
XX
XX Claim 11; Page 5218-5221; 5507pp; English.
XX
XX AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytostatic; hepatotropic; vulnery;
XX antiparasitic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
XX anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
XX cardiact; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
XX dermatological; immunosuppressive; antiinflammatory; antibacterial;
XX antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The
XX sequences can be used for determining the presence of or predisposition
XX to, or preventing or treating pathological conditions associated with an
XX ORFX-associated disorder. The nucleic acids can be used to express ORFX
XX proteins in gene therapy vectors. The proteins and nucleic acids may be
XX used to treat cancers, proliferative disorders, neurodegenerative
XX disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
XX diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
XX storage, systemic lupus erythematosus, severe combined immunodeficiency
XX (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
XX disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
XX cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
XX enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
XX SQ Sequence 1096 AA;
XX
XX Query Match 94.8%; Score 1178; DB 3; Length 1096;
XX Best Local Similarity 99.6%; Pred. No. 3.1e-123;
XX Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 13 QVDMLESEINIAPIRLTNFTGVMPQPKOLDLYLKTSPVTFPSDLSRNLYQVNEPGRNY 72
XX :|||||
XX 871 KYDMLSEINIAPIRLTNFTGVMPQPKOLDLYLKTSPVTFPSDLSRNLYQVNEPGRNY 930
XX
XX QY 73 NQQLNALVLYVGTOAIAHIHNKGSTPSNSTTTHSAHMDIFQNLAVDLDTGGRYLFUNA 132
XX :|||||
XX DB 931 NQQLNALVLYVGTOAIAHIHNKGSTPSNSTTTHSAHMDIFQNLAVDLDTGGRYLFUNA 990
XX
XX QY 133 ANQLRYPNSHTHYFSCMTLYLFAEANTEALQEQITRVLLERLIVNRPHPMGLITFIEL 192
XX :|||||
XX DB 991 ANQLRYPNSHTHYFSCMTLYLFAEANTEALQEQITRVLLERLIVNRPHPMGLITFIEL 1050
XX
XX QY 193 KNPAFFWNHEFVHCAPRIEKLFGSVAQCCMGOKQAQVMEGTGAS 238
XX :|||||
XX DB 1051 KNPAFFWNHEFVHCAPRIEKLFGSVAQCCMGOKQAQVMEGTGAS 1096
XX
XX
XX RESULT 6
XX ADQ96036
XX ID ADQ96036 standard; protein; 1553 AA.
XX
XX AC ADQ96036;
XX
XX DT 07-OCT-2004 (first entry)
XX

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DE T cell activation associated protein #107.
XX
XX antiallergic; antiarthritic; antiaesthetic; antidiabetic; anti-HIV;
XX antimicrobial; antirheumatic; immunosuppressive; neuroprotective;
XX gene therapy; T cell activation; diagnosis; autoimmune disease;
XX rheumatoid arthritis; asthma; multiple sclerosis; diabetes;
XX allergic disease; infectious disease; AIDS; chronic rejection; organ;
XX bone-marrow transplant.
XX
XX OS Homo sapiens.
XX
XX PN WO2004058805-A2.
XX
XX PD 15-JUL-2004.
XX
XX PF 25-DEC-2003; 2003MO-JP016715.
XX
XX PR 26-DEC-2002; 2002JP-00376365.
XX PR 27-DEC-2002; 2002US-0436473P.
XX PR 25-APR-2003; 2003JP-00122113.
XX PR 28-APR-2003; 2003US-0465792P.
XX PR 21-OCT-2003; 2003JP-00360559.
XX PR 22-OCT-2003; 2003US-0512846P.
XX
XX (ASAHI-) ASahi KASEI PHARMA CORP.
XX
XX PI Matbuda A, Yoneta S;
XX
XX DR WPI; 2004-593134/57.
XX DR N-PSDB; ADQ96035.
XX
XX PT New purified protein involved in T cell activation, useful for
XX diagnosing, preventing and/or treating acquired immunodeficiency
XX syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic
XX and infectious diseases.
XX
XX PS Claim 1; SEQ ID NO 214; 2828pp; English.
XX
XX CC The invention relates to purified proteins and genes encoding them, that
XX are involved in T cell activation (I) and has an amino acid deletion,
XX substitution or addition in the amino acid sequences. The methods and
XX compositions of the present invention are useful for the diagnosis,
XX prevention and/or treatment of autoimmune disease (rheumatoid arthritis,
XX asthma, multiple sclerosis and diabetes), allergic disease, infectious
XX disease, AIDS, and acute or chronic rejection at organ transplant or bone
XX marrow transplant. This sequence corresponds to a protein involved in T
XX cell activation.
XX
XX SQ Sequence 1553 AA;
XX
XX Query Match 94.8%; Score 1178; DB 8; Length 1553;
XX Best Local Similarity 99.6%; Pred. No. 5.2e-123;
XX Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 13 QVDMLESEINIAPIRLTNFTGVMPQPKOLDLYLKTSPVTFPSDLSRNLYQVNEPGRNY 72
XX :|||||
XX DB 1328 KYDMLSEINIAPIRLTNFTGVMPQPKOLDLYLKTSPVTFPSDLSRNLYQVNEPGRNY 1387
XX
XX QY 73 NQQLNALVLYVGTOAIAHIHNKGSTPSNSTTTHSAHMDIFQNLAVDLDTGGRYLFUNA 132
XX :|||||
XX DB 1388 NQQLNALVLYVGTOAIAHIHNKGSTPSNSTTTHSAHMDIFQNLAVDLDTGGRYLFUNA 1447
XX
XX QY 133 ANQLRYPNSHTHYFSCMTLYLFAEANTEALQEQITRVLLERLIVNRPHPMGLITFIEL 192
XX :|||||
XX DB 1448 ANQLRYPNSHTHYFSCMTLYLFAEANTEALQEQITRVLLERLIVNRPHPMGLITFIEL 1507
XX
XX QY 193 KNPAFFWNHEFVHCAPRIEKLFGSVAQCCMGOKQAQVMEGTGAS 238
XX :|||||
XX DB 1508 KNPAFFWNHEFVHCAPRIEKLFGSVAQCCMGOKQAQVMEGTGAS 1553
XX
XX
XX RESULT 7
XX AA02377
XX

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ID AAY02377 standard; protein; 1726 AA.
 AC AAY02377;
 DT 13-JUL-1999 (first entry)
 XX
 DE Polypeptide identified by the signal sequence trap method.
 KM Signal sequence trap method; SST method; immunisation; inhibition;
 KM infection; allergy; cancer; regulation; tissue formation; tissue repair;
 KM cytokine activity; inhibitor activity; chemokine activity;
 KM metabolic disorder; hormonal disorder; immune disorder; wound;
 KM severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer.
 XX Homo sapiens.
 OS
 PN WO918126-A1.
 XX
 PD 15-APR-1999.
 XX
 XX 06-OCT-1998; 98WO-JP004514.
 XX
 PR 07-OCT-1997; 97JP-00274674.
 XX
 PA (ONOV) ONO PHARM CO LTD.
 XX
 PI Fukushima D, Shibayama S, Tada H;
 DR WPI; 1999-277254/23.
 DR N-PSDB; AAX35732, AAX35733.
 XX
 PT Polypeptides identified by the signal sequence trap method from a human
 PT cDNA library.
 XX
 XX Claim 1; Page 178-186; 281pp; Japanese.
 XX
 CC AAY02358-84 represent novel polypeptides which are identified from a
 CC human placental cDNA library by the signal sequence trap (SST) method.
 CC The polypeptides are encoded by the cDNA sequences in AAX35694-X35747.
 CC CC immunisation against a broad range of physiological activity, including
 CC immunisation against and inhibition of infections, allergies and cancer;
 CC regulation of tissue formation and repair; activin/inhibin activity;
 CC chemokine/cytokine activity; blood coagulation regulation; and
 CC receptor/ligand agonist or antagonist activity. The polypeptides can be
 CC used for prevention and treatment of disorders including infections by
 CC bacteria, yeasts and viruses (including HIV) and protozoa; metabolic and
 CC hormonal disorders; immune disorders (including severe combined
 CC immunodeficiency (SCID) and AIDS; thrombosis; cancer; and traumatic or
 CC surgical wounds
 CC
 SQ Sequence 1726 AA;
 Query Match 94.8%; Score 1178; DB 2; Length 1726;
 Best Local Similarity 99.6%; Pred. No. 6e-123;
 Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QVDMLESEINAPRILNFTGVMPPOFKODLSYLTSPVTPFLSDLSNLOVSNPEPNRY 72
 DB 1501 KVDMLSEINAPRILNFTGVMPPOFKODLSYLTSPVTPFLSDLSNLOVSNPEPNRY 1560
 QY 73 NLQINLALVLYVGTQAIHAIHNKGSTPSMSTITHSAMDIPOMLAVDLDTGGRYLFPLNAI 132
 DB 1561 NLQINLALVLYVGTQAIHAIHNKGSTPSMSTITHSAMDIPOMLAVDLDTGGRYLFPLNAI 1620
 QY 133 ANOLRYNSHTHTFSCMTLYLPAEANTBAIOBOITRVLRLIYNRPHPGGLITPTELI 192
 DB 1621 ANOLRYNSHTHTFSCMTLYLPAEANTBAIOBOITRVLRLIYNRPHPGGLITPTELI 1680
 QY 193 KNPAPFKFNNHBFVHCAPRIEKLFPQSVAAOCMGOKOAOVMEGTGAS 238
 DB 1681 KNPAPFKFNNHBFVHCAPRIEKLFPQSVAAOCMGOKOAOVMEGTGAS 1726

RESULT 8
 ID ABB81196 standard; protein; 2141 AA.
 AC ABB81196;
 DT 25-NOV-2002 (first entry)
 XX
 DE Human PNI3734 protein sequence.
 KM SET; PNI2218; TTP; CIN85; PNI3734; TIAR; FUBP1; antiinflammatory;
 KM antiarteriosclerotic; cardiact; neurotropic; gene therapy; human.
 XX
 OS Homo sapiens.
 OS
 PN WO200264733-A2.
 XX
 PD 22-AUG-2002.
 XX
 XX 14-DEC-2001; 2001WO-US047655.
 XX
 PR 14-DEC-2000; 2000US-0255063P.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Cimborra DM, Heichman K, Bartel PL;
 DR WPI; 2002-643476/69.
 DR N-PSDB; ABQ79531.
 XX
 PT New isolated protein complex comprising a first and second protein,
 PT useful for the diagnosis and treatment of disorders involved in the
 PT protein-protein interaction, such as inflammatory disease,
 PT atherosclerosis or hypoxic brain injury.
 XX
 XX Claim 117; Page 23-24; 77pp; English.
 XX
 CC The invention relates to an isolated protein complex comprising 2
 CC proteins. The protein complex comprises: (a) a first protein (P1) and a
 CC second protein (P2); (b) a fragment P1 and P2; (c) P1 and a fragment P2;
 CC and (d) a fragment of P1 and a fragment P2. The first and second proteins
 CC of the complex are selected from: (i) P1 is SET, and P2 is PNI2218; (ii)
 CC P1 is TTP and P2 is CIN85 or PNI3734; or (iii) P1 is TIAR and P2 is
 CC FUBP1. The methods and compositions of the present invention are useful
 CC for the diagnosis and/or treatment of physiological disorders involved in
 CC the protein-protein interaction, such as inflammatory disease,
 CC atherosclerosis, cardiac hypertrophy, or hypoxic brain injury. The drugs,
 CC modulators, inhibitor or compounds are useful for treating the diseases
 CC described above. The present sequence represents the predicted amino acid
 CC sequence of PNI3734
 CC
 SQ Sequence 2141 AA;
 Query Match 94.8%; Score 1178; DB 5; Length 2141;
 Best Local Similarity 99.6%; Pred. No. 8.3e-123;
 Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QVDMLESEINAPRILNFTGVMPPOFKODLSYLTSPVTPFLSDLSNLOVSNPEPNRY 72
 DB 1916 KVDMLSEINAPRILNFTGVMPPOFKODLSYLTSPVTPFLSDLSNLOVSNPEPNRY 1975
 QY 73 NLQINLALVLYVGTQAIHAIHNKGSTPSMSTITHSAMDIPOMLAVDLDTGGRYLFPLNAI 132
 DB 1976 NLQINLALVLYVGTQAIHAIHNKGSTPSMSTITHSAMDIPOMLAVDLDTGGRYLFPLNAI 2035
 QY 133 ANOLRYNSHTHTFSCMTLYLPAEANTBAIOBOITRVLRLIYNRPHPGGLITPTELI 192
 DB 2036 ANOLRYNSHTHTFSCMTLYLPAEANTBAIOBOITRVLRLIYNRPHPGGLITPTELI 2095
 QY 193 KNPAPFKFNNHBFVHCAPRIEKLFPQSVAAOCMGOKOAOVMEGTGAS 238
 DB 2096 KNPAPFKFNNHBFVHCAPRIEKLFPQSVAAOCMGOKOAOVMEGTGAS 2141

```
RESULT 9
ID ABR58313 standard; protein; 2376 AA.
XX
AC ABR58313;
XX
DT 08-JUL-2003 (first entry)
XX
DE BC00586 protein #SEQ ID 72.
XX
KW Breast cancer; cytostatic; gene therapy; antisense therapy; regulated;
KM drug discovery; clinical medicine; forensic medicine; chromosome 16q13.
XX
OS Homo sapiens.
XX
PN WO2003029421-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031287.
XX
PR 03-OCT-2001; 2001US-0326526P.
PR 14-MAY-2002; 2002US-00144194.
XX
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
PI Sun Z, Li X, Fan W, Kovacs KF, Jay G;
XX
DR WPI; 2003-381623/36.
DR N-PSDB; ACC72047.
XX
PT New isolated human differentially-regulated breast cancer polynucleotide
PT and polypeptide, useful for diagnosing, staging, prognosticating,
PT preventing and/or treating diseases and conditions relating to breast
PT cancer.
XX
PS Claim 6; SEQ ID NO 72; 127pp + Sequence listing; English.
XX
CC The invention relates to isolated polynucleotides which are
CC differentially-regulated in breast cancer. The methods and compositions
CC of the present invention are useful for detecting, diagnosing, staging,
CC monitoring, prognosticating, preventing and/or treating diseases and
CC conditions relating to breast cancer, and may be used in gene therapy or
CC antisense therapy. They can also be used in research, drug discovery,
CC clinical medicine and forensic medicine. Sequences given in records
CC ABR58278-ABR58323 and ABR58346-ABR58362 represent polypeptides encoded by
CC polynucleotides of the invention that are differentially-regulated in
CC breast cancer. NOTE: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pcc_sequences
XX
SQ Sequence 2376 AA;
XX
Query Match 94.8%; Score 1178; DB 6; Length 2376;
Best Local Similarity 99.6%; Pred. No. 9.7e-123;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 13 QVDMLESEINIAPIRLTNFTGVPMPQPKDLSYLTSTRSPVTLSDLRSLQVSNBGRNY 72
:|||||
DB 2151 KVDMLSEINIAPIRLTNFTGVPMPQPKDLSYLTSTRSPVTLSDLRSLQVSNBGRNY 2210
QY 73 NQOLINALVLYGTQAIHAIHNKGSTPSNSTTTHSAHMDIFQNLAVDLDTBGRYLFNLAI 132
:|||||
DB 2211 NQOLINALVLYGTQAIHAIHNKGSTPSNSTTTHSAHMDIFQNLAVDLDTBGRYLFNLAI 2270
QY 133 ANOLRPNSHTHFTSCMTLYLPAEANTBAIOEITVTLERLLVNRPHMGILITPILAI 192
:|||||
DB 2271 ANOLRPNSHTHFTSCMTLYLPAEANTBAIOEITVTLERLLVNRPHMGILITPILAI 2330
QY 193 KNPAPFWMHBFVHCAPBIEIKLFQSYAQCCKGQKQAOQWEGTGAS 238
:|||||
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```
DB 2331 KNPAPFWMHBFVHCAPBIEIKLFQSYAQCCKGQKQAOQWEGTGAS 2376
XX
RESULT 10
ID ADQ96034 standard; protein; 2376 AA.
XX
AC ADQ96034;
XX
DT 07-OCT-2004 (first entry)
XX
DE T cell activation associated protein #106.
XX
KW antiallergic; antiarthritic; antiasthmatic; antidiabetic; anti-HIV;
KM antimicrobial; antirheumatic; immunosuppressive; neuroprotective;
KM gene therapy; T cell activation; diagnosis; autoimmune disease;
KM rheumatoid arthritis; asthma; multiple sclerosis; diabetes;
KM allergic disease; infectious disease; AIDS; chronic rejection; organ;
KM bone-marrow transplant.
XX
OS Homo sapiens.
XX
PN WO2004058805-A2.
XX
PD 15-JUL-2004.
XX
PF 25-DEC-2003; 2003WO-JP016715.
XX
PR 26-DEC-2002; 2002JP-00376365.
PR 27-DEC-2002; 2002US-0436473P.
PR 25-APR-2003; 2003JP-00122113.
PR 28-APR-2003; 2003US-0465792P.
PR 21-OCT-2003; 2003JP-00360559.
PR 22-OCT-2003; 2003US-0512846P.
XX
PA (ASAH-) ASAMI KASEI PHARMA CORP.
XX
PI Matsuda A, Yoneta S;
XX
DR WPI; 2004-593134/57.
DR N-PSDB; ADQ96033.
XX
PT New purified protein involved in T cell activation, useful for
PT diagnosing, preventing and/or treating acquired immunodeficiency
PT syndrome, autoimmune (e.g. rheumatoid arthritis, and diabetes), allergic
PT and infectious diseases.
XX
XX
XX Claim 1; SEQ ID NO 212; 2828pp; English.
XX
CC The invention relates to purified proteins and genes encoding them, that
CC are involved in T cell activation (I) and has an amino acid deletion,
CC substitution or addition in the amino acid sequences. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of autoimmune disease (rheumatoid arthritis,
CC asthma, multiple sclerosis and diabetes), allergic disease, infectious
CC disease, AIDS, and acute or chronic rejection at organ transplant or bone
CC -marrow transplant. This sequence corresponds to a protein involved in T
CC cell activation.
XX
SQ Sequence 2376 AA;
XX
Query Match 94.8%; Score 1178; DB 8; Length 2376;
Best Local Similarity 99.6%; Pred. No. 9.7e-123;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 13 QVDMLESEINIAPIRLTNFTGVPMPQPKDLSYLTSTRSPVTLSDLRSLQVSNBGRNY 72
:|||||
DB 2151 KVDMLSEINIAPIRLTNFTGVPMPQPKDLSYLTSTRSPVTLSDLRSLQVSNBGRNY 2210
QY 73 NQOLINALVLYGTQAIHAIHNKGSTPSNSTTTHSAHMDIFQNLAVDLDTBGRYLFNLAI 132
:|||||
DB 2211 NQOLINALVLYGTQAIHAIHNKGSTPSNSTTTHSAHMDIFQNLAVDLDTBGRYLFNLAI 2270
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Qy 133 ANQLRPNSTHTYFSCMTLYLFAEANTAEALQEOITRVLLERLIYNRPHPGLITITPELI 192
    |||
Db 2271 ANQLRPNSTHTYFSCMTLYLFAEANTAEALQEOITRVLLERLIYNRPHPGLITITPELI 2330
    |||

Qy 193 KNPAFKFMNHEFVHCAPEIEKLFGSVACCGMGOQAQOVWEGTAS 238
    |||
Db 2331 KNPAFKFMNHEFVHCAPEIEKLFGSVACCGMGOQAQOVWEGTAS 2376
    |||

RESULT 11
ADQ08792
ID ADQ08792 standard; protein; 1167 AA.
XX
XX ADQ08792;
AC
XX
XX 26-AUG-2004 (first entry)
XX
XX Ciona intestinalis nervous system associated protein SegID:194.
DE
XX
XX gene cluster; nervous system; sea-squirt tailbud; embryo; larva;
XX nervous system disease.
XX
XX Ciona intestinalis.
XX
XX JP2004057127-A.
XX
XX 26-FEB-2004.
XX
XX 31-JUL-2002; 2002JP-00222532.
XX
XX 31-JUL-2002; 2002JP-00222532.
XX
XX 31-JUL-2002; 2002JP-00222532.
XX
XX (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.
XX
XX WPI; 2004-208712/20.
XX
XX N-PSDB; ADQ08791.
XX
XX Novel genes derived from Ciona intestinalis (sea squirt), expressed in
XX nervous system in the tailbud embryo or larva, useful for studying the
XX development of nervous system.
XX
XX Claim 4; SEQ ID NO 194; 897pp; Japanese.
XX
XX This invention relates to a novel gene cluster, where the encoded
XX proteins are expressed in the nervous system of sea-squirt tailbud embryo
XX or larva. The invention is useful for studying the development of the
XX nervous system of the sea-squirt and for research purposes. The genes may
XX be used for determining the disease-development mechanisms in the nervous
XX system. In addition, novel gene clusters expressed in nervous system of
XX sea-squirt tailbud embryo or larva allows development of diagnostics and
XX therapeutics related to nervous system diseases. The present sequence is
XX that of a protein encoded by a C intestinalis gene of the invention.
XX
XX Sequence 1167 AA;
SQ
Query Match 79.1%; Score 983; DB 8; Length 1167;
Best Local Similarity 81.4%; Pred. No. 3.8e-101;
Matches 184; Conservative 22; Mismatches 20; Indels 0; Gaps 0;
Qy 13 OVDMLSEINIAPIRLITNFGVMPPOPKDLSYLTKTRSPVTFSLDSRLSNLOVNBGNRY 72
    |||
Db 931 KVDMLSEINIAPIRLITNFGVMPPOPKDLSYLTKTRSPVTFSLDSRLSNLOVNBGNRY 990
    |||

Qy 73 NGLINAVLVYGTGTOAIAHINKGSTPSMSTITHSAHMDIFONLAVDLDTGRYLFMAI 132
    |||
Db 991 NGLINAVLVYGTGTOAIAHINKGSTPSMSTITHSHMDIFONLAVDLDTGRYLFMAI 1050
    |||

Qy 133 ANQLRPNSTHTYFSCMTLYLFAEANTAEALQEOITRVLLERLIYNRPHPGLITITPELI 192
    |||
Db 1051 ANQLRPNSTHTYFSCMTLYLFAEANTAEALQEOITRVLLERLIYNRPHPGLITITPELI 1110
    |||

Qy 193 KNPAFKFMNHEFVHCAPEIEKLFGSVACCGMGOQAQOVWEGTAS 238
    |||

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Db 1111 KNPAFKFMNHEFVHCAPEIEKLFGSVARSCMGKQFTQGVTDTRATT 1156
    |||

RESULT 12
ABG04093
ID ABG04093 standard; protein; 354 AA.
XX
XX ABG04093;
AC
XX
XX 13-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #4084.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX NC200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001MO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSB-) HYSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS68280.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 34452; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp://ipo.int/pub/published_pct_sequences
XX
XX Sequence 354 AA;
SQ
Query Match 79.0%; Score 982; DB 4; Length 354;
Best Local Similarity 95.5%; Pred. No. 8.4e-102;
Matches 190; Conservative 2; Mismatches 5; Indels 2; Gaps 2;
Qy 13 OVDMLSEINIAPIRLITNFGVMPPOPKDLSYLTKTRSPVTFSLDSRLSNLOVNBGNRY 72
    |||
Db 156 KVDMLSEINIAPIRLITNFGVMPPOPKDLSYLTKTRSPVTFSLDSRLSNLOVNBGNRY 215
    |||

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QY 73 NQQLNALVLYVGTQAIHINHGKSTPSMSTITHSAHMDIFQNLAVDLDTBGRYLFNLAI 132
 DB 216 NQQLNALVLYVGTQAIHINHGKSTPSMSTITHSAHMDIFQNLAVDLDTBGRYLFNLAI 275
 QY 133 ANQLRYPNSHTYFSCYMLYFAEANT-EALQEQITRVLLERLIYNRPHPWGLITFIEL 190
 DB 276 ANQLRYPNSHTYFSCYMLYFGRRANSGRPFQEQITRVLLERLIYNRPHPWGLITFIEL 335
 QY 191 LKRPAPKFMNHEFYHCAP 209
 DB 336 LKRPAPKFMNHEFYHCAP 354

RESULT 13

AA093552
 ID AA093552 standard; protein; 873 AA.

AC AAM93552;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide, SEQ ID NO: 3315.
 XX
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX
 OS Homo sapiens.
 XX
 PN EP130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-00114089.
 XX
 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-0018774.
 PR 02-MAY-2000; 2000JP-00183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR WPI; 2001-524255/58.
 DR N-PSDB; AAK94484.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PS Claim 8; SEQ ID NO 3315; 1380bp + Sequence Listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesized by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX
 SQ Sequence 873 AA;

Query Match 76.5%; Score 951; DB 4; Length 873;
 Best Local Similarity 99.5%; Pred. No. 1e-97;
 Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QYDMLSEINIAPRIILNFTGWPMPQPKODLSYLKTRSPVTFISDLRSNLQVSNBPNRY 72
 DB 689 KQDMLSEINIAPRIILNFTGWPMPQPKODLSYLKTRSPVTFISDLRSNLQVSNBPNRY 748

QY 73 NQQLNALVLYVGTQAIHINHGKSTPSMSTITHSAHMDIFQNLAVDLDTBGRYLFNLAI 132
 DB 749 NQQLNALVLYVGTQAIHINHGKSTPSMSTITHSAHMDIFQNLAVDLDTBGRYLFNLAI 808
 QY 133 ANQLRYPNSHTYFSCYMLYFAEANT-EALQEQITRVLLERLIYNRPHPWGLITFIEL 192
 DB 809 ANQLRYPNSHTYFSCYMLYFAEANT-EALQEQITRVLLERLIYNRPHPWGLITFIEL 868
 QY 193 KNPAP 197
 DB 869 KNPAP 873

RESULT 14

ADL31282
 ID ADL31282 standard; protein; 873 AA.

AC ADL31282;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human protein encoded by a full length cDNA clone SeqID 3315.
 XX
 KW human; medicine; signal transduction; glycoprotein; transcription;
 KW oligo-capping method.
 XX
 OS Homo sapiens.
 XX
 PN EP1396543-A2.
 XX
 PD 10-MAR-2004.
 XX
 PF 07-JUL-2000; 2003EP-00025638.
 XX
 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-0018774.
 PR 02-MAY-2000; 2000JP-00183865.
 PR 07-JUL-2000; 2000EP-00114089.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR WPI; 2004-204755/20.
 DR N-PSDB; ADL31281.
 XX
 PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full
 PT length human cDNAs.
 PS Example 1; SEQ ID NO 3315; 1340bp; English.
 XX
 CC This invention relates to a novel primers useful for synthesizing full
 CC length cDNA molecules that encode human proteins. Specifically, it refers
 CC to secretory or membrane proteins that are potential therapeutic agents/
 CC target molecules in the field of medicine, and in particular genes
 CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'
 CC ends using the oligo-capping method. This polypeptide sequence is a full
 CC length human protein of the invention.
 XX
 SQ Sequence 873 AA;

Query Match 76.5%; Score 951; DB 8; Length 873;
 Best Local Similarity 99.5%; Pred. No. 1e-97;
 Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QYDMLSEINIAPRIILNFTGWPMPQPKODLSYLKTRSPVTFISDLRSNLQVSNBPNRY 72
 DB 689 KQDMLSEINIAPRIILNFTGWPMPQPKODLSYLKTRSPVTFISDLRSNLQVSNBPNRY 748
 QY 73 NQQLNALVLYVGTQAIHINHGKSTPSMSTITHSAHMDIFQNLAVDLDTBGRYLFNLAI 132

Db 749 NLGLINLVLYGVQALAHINKGSTPSMSTITSAHMDIFQNLAVDITGRIYLFNAI 808
Qy 133 ANQLRYPNSHTHYFSCMTLYIPAEANTEALIOEQITRVLLERLIYNRPHPWGLITPIELI 192
Db 809 ANQLRYPNSHTHYFSCMTLYIPAEANTEALIOEQITRVLLERLIYNRPHPWGLITPIELI 868
Qy 193 KNPAF 197
Db 869 KNPAF 873

RESULT 15

ABB58631
ID ABB58631 standard; protein; 1766 AA.

AC ABB58631;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 2685.

KM Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.

OS Drosophila melanogaster.

PN M0200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001MO-US009231.

PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li FWD, Myers EW;

DR WPI; 2001-656860/75.
N-PSDB; ABL02734.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions.

PS Disclosure; SEQ ID NO 2685; 21pp + Sequence listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
sequences (ABB72072) and the encoded proteins (ABB57737-
ABB72072). The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1766 AA;

Query Match 70.2%; Score 873; DB 4; Length 1766;

Best Local Similarity 71.7%; Pred. No. 2e-88;
Matches 165; Conservative 30; Mismatches 29; Indels 6; Gaps 2;

Qy 13 QVDMLSRINTAPRLTNP-TGVMPQPKQLDSYLTGRSPVTPFLSDLRSLQVSNRGNR 71

Db 1530 KVDMLSDSSNAKPKLSSYINQIPANKKQDLSYLTGRAPVTFLSKRGHLQVTSRPGTR 1589

Qy 72 YNLQILNALVLYVGTQALAHINKGSTPSMSTITSAHMDIFQNLAVDITGRIYLFNAI 131

Db 1590 YNMAIMNALVMYVGTQALAHIRKKNFVPNTSNIAHSAHMDIFQNLAVDITGRIYLFNAI 1649

Qy 132 IANQLRYPNSHTHYFSCMTLYIPAEANTEALIOEQITRVLLERLIYNRPHPWGLITPIELI 191
Db 1650 IANQLRYPNSHTHYFSCAVLHLFAEANSALIOEQITRVLLERLIYNRPHPWGLITPIELI 1709
Qy 192 KNPAFKNHBEFVHCAPETIEKLFGSVACCMGQKAQ-----VMEGTG 236
Db 1710 IKNPITYKFDHDFVHCAPETITKLFGSVARSCIAKSNVTQQLNMPVVDGEG 1759

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OM protein - protein search, using sw model

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Title: US-10-019-151c-1

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Searched: 1726220 seqs, 38632138 residues

Total number of hits satisfying chosen parameters: 1726220

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178	94.8	1070	US-10-094-749-2853	Sequence 2853, Ap
2	1178	94.8	1726	US-08-529-063-58	Sequence 58, Appl
3	1178	94.8	1726	US-10-414-378-58	Sequence 58, Appl
4	1178	94.8	2141	US-10-014-814-6	Sequence 6, Appl
5	1178	94.8	2141	US-10-690-276-10	Sequence 10, Appl
6	1178	94.8	2376	US-10-144-194A-72	Sequence 72, Appl
7	1178	94.8	2376	US-10-491-566-72	Sequence 72, Appl
8	653	52.5	2500	US-10-369-493-5760	Sequence 5760, Ap
9	648.5	52.2	394	US-10-424-599-180820	Sequence 180820, Ap
10	641	51.6	683	US-10-425-114-59023	Sequence 59023, A
11	641	51.6	819	US-10-425-114-70535	Sequence 70535, A

12	641	51.6	860	16	US-10-425-115-192123	Sequence 192123, A
13	635	51.1	215	15 <td>US-10-425-114-53929</td> <td>Sequence 53929, A</td>	US-10-425-114-53929	Sequence 53929, A
14	617.5	49.7	443	15 <td>US-10-425-115-192119</td> <td>Sequence 192119, A</td>	US-10-425-115-192119	Sequence 192119, A
15	616.5	49.6	443	15 <td>US-10-425-114-37764</td> <td>Sequence 37764, A</td>	US-10-425-114-37764	Sequence 37764, A
16	609.5	49.0	2396	16 <td>US-10-437-963-122555</td> <td>Sequence 122555, A</td>	US-10-437-963-122555	Sequence 122555, A
17	581.5	46.8	178	10 <td>US-09-768-235R-6</td> <td>Sequence 6, Appl</td>	US-09-768-235R-6	Sequence 6, Appl
18	547.5	44.0	203	16 <td>US-10-437-963-199167</td> <td>Sequence 199167, A</td>	US-10-437-963-199167	Sequence 199167, A
19	461.5	37.1	167	16 <td>US-10-767-701-50233</td> <td>Sequence 50233, A</td>	US-10-767-701-50233	Sequence 50233, A
20	373	30.0	176	16 <td>US-10-767-701-51806</td> <td>Sequence 51806, A</td>	US-10-767-701-51806	Sequence 51806, A
21	356.5	28.7	1283	15 <td>US-10-369-493-13367</td> <td>Sequence 13367, A</td>	US-10-369-493-13367	Sequence 13367, A
22	318.5	25.6	2016	17 <td>US-10-741-849-7229</td> <td>Sequence 7229, Ap</td>	US-10-741-849-7229	Sequence 7229, Ap
23	317	25.5	2100	15 <td>US-10-369-493-2142</td> <td>Sequence 2142, Ap</td>	US-10-369-493-2142	Sequence 2142, Ap
24	295	23.7	89	15 <td>US-10-425-114-38183</td> <td>Sequence 38183, A</td>	US-10-425-114-38183	Sequence 38183, A
25	256	20.6	1610	15 <td>US-10-369-493-3448</td> <td>Sequence 3448, Ap</td>	US-10-369-493-3448	Sequence 3448, Ap
26	247.5	19.9	103	16 <td>US-10-425-115-291245</td> <td>Sequence 291245, A</td>	US-10-425-115-291245	Sequence 291245, A
27	231.5	18.6	2108	15 <td>US-10-369-493-1537</td> <td>Sequence 1537, Ap</td>	US-10-369-493-1537	Sequence 1537, Ap
28	195	15.7	58	16 <td>US-10-767-701-37027</td> <td>Sequence 37027, A</td>	US-10-767-701-37027	Sequence 37027, A
29	169.5	13.6	172	16 <td>US-10-437-963-115561</td> <td>Sequence 115561, A</td>	US-10-437-963-115561	Sequence 115561, A
30	166.5	13.4	105	16 <td>US-10-425-115-213731</td> <td>Sequence 213731, A</td>	US-10-425-115-213731	Sequence 213731, A
31	166	13.4	77	15 <td>US-10-424-599-248161</td> <td>Sequence 248161, A</td>	US-10-424-599-248161	Sequence 248161, A
32	163	13.1	56	16 <td>US-10-767-701-47530</td> <td>Sequence 47530, A</td>	US-10-767-701-47530	Sequence 47530, A
33	110.5	8.9	49	16 <td>US-10-425-115-332119</td> <td>Sequence 332119, A</td>	US-10-425-115-332119	Sequence 332119, A
34	88.5	7.1	410	15 <td>US-10-282-1228-61422</td> <td>Sequence 61422, A</td>	US-10-282-1228-61422	Sequence 61422, A
35	87.5	7.0	416	16 <td>US-10-425-115-336084</td> <td>Sequence 336084, A</td>	US-10-425-115-336084	Sequence 336084, A
36	87.5	7.0	423	15 <td>US-10-425-115-58542</td> <td>Sequence 58542, A</td>	US-10-425-115-58542	Sequence 58542, A
37	87.5	7.0	4624	16 <td>US-10-408-765A-29291</td> <td>Sequence 29291, Ap</td>	US-10-408-765A-29291	Sequence 29291, Ap
38	86.5	7.0	1443	16 <td>US-10-437-963-151795</td> <td>Sequence 151795, A</td>	US-10-437-963-151795	Sequence 151795, A
39	86.5	7.0	1538	16 <td>US-10-437-963-151793</td> <td>Sequence 151793, A</td>	US-10-437-963-151793	Sequence 151793, A
40	86	6.9	4104	15 <td>US-10-282-1228-70280</td> <td>Sequence 70280, A</td>	US-10-282-1228-70280	Sequence 70280, A
41	85.5	6.9	400	16 <td>US-10-425-115-220152</td> <td>Sequence 220152, A</td>	US-10-425-115-220152	Sequence 220152, A
42	85.5	6.9	657	15 <td>US-10-425-114-55558</td> <td>Sequence 55558, A</td>	US-10-425-114-55558	Sequence 55558, A
43	85.5	6.9	658	15 <td>US-10-424-599-188855</td> <td>Sequence 188855, A</td>	US-10-424-599-188855	Sequence 188855, A
44	84.5	6.8	679	15 <td>US-10-295-027-1222</td> <td>Sequence 1222, Ap</td>	US-10-295-027-1222	Sequence 1222, Ap
45	84.5	6.8	679	15 <td>US-10-108-260A-4563</td> <td>Sequence 4563, Ap</td>	US-10-108-260A-4563	Sequence 4563, Ap

ALIGNMENTS

RESULT 1
US-10-094-749-2853
; Sequence 2853, Application US/10094749
; Publication No. US20030219741A1
GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUKIO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKI
; APPLICANT: NAGAHARA, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094, 749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350, 435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3181
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2853

LENGTH: 1070
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2853

Query Match 94.8%; Score 1178; DB 15; Length 1070;
Best Local Similarity 99.6%; Pred. No. 1.1e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

13 QVDMLESEINIAPIRLNFTGVPMPQPKDLSYLKTRSPVTFSLDRSNLQVSNBGNRY 72
:|||||
845 KVDMLSEINIAPIRLNFTGVPMPQPKDLSYLKTRSPVTFSLDRSNLQVSNBGNRY 904
|||
QY 73 NQOLINALVLYGTOAIAIHNGKSTPMSSTITHSAHMDIFONLAVDLDTREGYLFPLNAI 132
|||||
DB 905 NQOLINALVLYGTOAIAIHNGKSTPMSSTITHSAHMDIFONLAVDLDTREGYLFPLNAI 964
|||||
QY 133 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 192
|||||
DB 965 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 1024
|||||
QY 193 KNPAKFMNHEFVHCAPEIEKLFQSVAAQCCMGOKQAQVWEGTGAS 238
|||||
DB 1025 KNPAKFMNHEFVHCAPEIEKLFQSVAAQCCMGOKQAQVWEGTGAS 1070
|||||

RESULT 2
US-09-529-063-58
Sequence 58, Application US/09529063
Patent No. US20020102542A1

GENERAL INFORMATION:
APPLICANT: FUKUSHIMA, DAICHI
APPLICANT: SHIBAYAMA, SHIRO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF
FILE REFERENCE: Q58769
CURRENT APPLICATION NUMBER: US/09/529,063
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: PCT/JP98/04514
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: JP 9-274674
PRIOR FILING DATE: 1997-10-07
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 1726
TYPE: PRT
ORGANISM: Homo sapiens
US-09-529-063-58

Query Match 94.8%; Score 1178; DB 9; Length 1726;
Best Local Similarity 99.6%; Pred. No. 2.2e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

13 QVDMLESEINIAPIRLNFTGVPMPQPKDLSYLKTRSPVTFSLDRSNLQVSNBGNRY 72
:|||||
DB 1501 KVDMLSEINIAPIRLNFTGVPMPQPKDLSYLKTRSPVTFSLDRSNLQVSNBGNRY 1560
|||||
QY 73 NQOLINALVLYGTOAIAIHNGKSTPMSSTITHSAHMDIFONLAVDLDTREGYLFPLNAI 132
|||||
DB 1561 NQOLINALVLYGTOAIAIHNGKSTPMSSTITHSAHMDIFONLAVDLDTREGYLFPLNAI 1620
|||||
QY 133 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 192
|||||
DB 1621 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 1680
|||||
QY 193 KNPAKFMNHEFVHCAPEIEKLFQSVAAQCCMGOKQAQVWEGTGAS 238
|||||
DB 1681 KNPAKFMNHEFVHCAPEIEKLFQSVAAQCCMGOKQAQVWEGTGAS 1726
|||||

RESULT 3

US-10-414-378-58
Sequence 58, Application US/10414378
Publication No. US20030016598A1

GENERAL INFORMATION:
APPLICANT: FUKUSHIMA, DAICHI
APPLICANT: SHIBAYAMA, SHIRO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE POLYPEPTIDE, AND USE OF
FILE REFERENCE: Q58769
CURRENT APPLICATION NUMBER: US/10/414,378
PRIOR FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: US/09/529,063
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: PCT/JP98/04514
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: JP 9-274674
PRIOR FILING DATE: 1997-10-07
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 1726
TYPE: PRT
ORGANISM: Homo sapiens
US-10-414-378-58

Query Match 94.8%; Score 1178; DB 14; Length 1726;
Best Local Similarity 99.6%; Pred. No. 2.2e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

13 QVDMLESEINIAPIRLNFTGVPMPQPKDLSYLKTRSPVTFSLDRSNLQVSNBGNRY 72
:|||||
DB 1501 KVDMLSEINIAPIRLNFTGVPMPQPKDLSYLKTRSPVTFSLDRSNLQVSNBGNRY 1560
|||||
QY 73 NQOLINALVLYGTOAIAIHNGKSTPMSSTITHSAHMDIFONLAVDLDTREGYLFPLNAI 132
|||||
DB 1561 NQOLINALVLYGTOAIAIHNGKSTPMSSTITHSAHMDIFONLAVDLDTREGYLFPLNAI 1620
|||||
QY 133 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 192
|||||
DB 1621 ANGLRYPNSHTYFSCMTLYLPABANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 1680
|||||
QY 193 KNPAKFMNHEFVHCAPEIEKLFQSVAAQCCMGOKQAQVWEGTGAS 238
|||||
DB 1681 KNPAKFMNHEFVHCAPEIEKLFQSVAAQCCMGOKQAQVWEGTGAS 1726
|||||

RESULT 4
US-10-014-814-6
Sequence 6, Application US/10014814
Publication No. US20030032058A1

GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Cimbora, Daniel M.
APPLICANT: Heichman, Karen
APPLICANT: Bartel, Paul L.
TITLE OF INVENTION: Protein-Protein Interactions
FILE REFERENCE: 2318-277-II
CURRENT APPLICATION NUMBER: US/10/014,814
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/255,063
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 2141
TYPE: PRT
ORGANISM: Homo sapiens
US-10-014-814-6

Query Match 94.8%; Score 1178; DB 14; Length 2141;
Best Local Similarity 99.6%; Pred. No. 3e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 13 QVDMLSRINIAPIRLTNFTGVPMPQPKDLDYLTKTRSPVTPLSDLRSLQVSNBGNRY 72
:|||||
DB 1916 KVMLSRINIAPIRLTNFTGVPMPQPKDLDYLTKTRSPVTPLSDLRSLQVSNBGNRY 1975
QY 73 NQOLINALVLYVGTQAIHAIHNKGSTPSMSTITHSAAMDIFONLAVDLDTBGRYLFNLAI 132
|||||
DB 1976 NQOLINALVLYVGTQAIHAIHNKGSTPSMSTITHSAAMDIFONLAVDLDTBGRYLFNLAI 2035
QY 133 ANQLRYPNSHTHYFSCCTMLYLPFAEANTEAIOEQITRVLLERLIVNRPHPMGLITFIETI 192
|||||
DB 2036 ANQLRYPNSHTHYFSCCTMLYLPFAEANTEAIOEQITRVLLERLIVNRPHPMGLITFIETI 2095
QY 193 KNPAKFMNHEFVHCAPBIEIKLFGSVAQCCMGOKAQOQVMEGTGAS 238
|||||
DB 2096 KNPAKFMNHEFVHCAPBIEIKLFGSVAQCCMGOKAQOQVMEGTGAS 2141

RESULT 5
US-10-690-276-10
; Sequence 10, Application US/10690276
; Publication No. US20050112118A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Incorporated
; APPLICANT: Climbora, Daniel
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul
; APPLICANT: Mauck, Kimberly
; APPLICANT: Bush, Angie
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
; FILE REFERENCE: 1834.01
; CURRENT APPLICATION NUMBER: US/10/690,276
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/727,384
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/168,377
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/168,379
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/185,056
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 10/035,344
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,571
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/035,343
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,572
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/099,924
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,179
; PRIOR FILING DATE: 2001-03-15
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 728
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2141
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-690-276-10

Query Match 94.8%; Score 1178; DB 17; Length 2141;
Best Local Similarity 99.6%; Pred. No. 3e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLSRINIAPIRLTNFTGVPMPQPKDLDYLTKTRSPVTPLSDLRSLQVSNBGNRY 72
:|||||
DB 1916 KVMLSRINIAPIRLTNFTGVPMPQPKDLDYLTKTRSPVTPLSDLRSLQVSNBGNRY 1975
QY 73 NQOLINALVLYVGTQAIHAIHNKGSTPSMSTITHSAAMDIFONLAVDLDTBGRYLFNLAI 132
|||||
DB 1976 NQOLINALVLYVGTQAIHAIHNKGSTPSMSTITHSAAMDIFONLAVDLDTBGRYLFNLAI 2035
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QY 133 ANQLRYPNSHTHYFSCCTMLYLPFAEANTEAIOEQITRVLLERLIVNRPHPMGLITFIETI 192
|||||
DB 2036 ANQLRYPNSHTHYFSCCTMLYLPFAEANTEAIOEQITRVLLERLIVNRPHPMGLITFIETI 2095
QY 193 KNPAKFMNHEFVHCAPBIEIKLFGSVAQCCMGOKAQOQVMEGTGAS 238
|||||
DB 2096 KNPAKFMNHEFVHCAPBIEIKLFGSVAQCCMGOKAQOQVMEGTGAS 2141

RESULT 6
US-10-144-194A-72
; Sequence 72, Application US/10144194A
; Publication No. US20030215809A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/144,194A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 2376
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-144-194A-72

Query Match 94.8%; Score 1178; DB 15; Length 2376;
Best Local Similarity 99.6%; Pred. No. 3.4e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLSRINIAPIRLTNFTGVPMPQPKDLDYLTKTRSPVTPLSDLRSLQVSNBGNRY 72
:|||||
DB 2151 KVMLSRINIAPIRLTNFTGVPMPQPKDLDYLTKTRSPVTPLSDLRSLQVSNBGNRY 2210
QY 73 NQOLINALVLYVGTQAIHAIHNKGSTPSMSTITHSAAMDIFONLAVDLDTBGRYLFNLAI 132
|||||
DB 2211 NQOLINALVLYVGTQAIHAIHNKGSTPSMSTITHSAAMDIFONLAVDLDTBGRYLFNLAI 2270
QY 133 ANQLRYPNSHTHYFSCCTMLYLPFAEANTEAIOEQITRVLLERLIVNRPHPMGLITFIETI 192
|||||
DB 2271 ANQLRYPNSHTHYFSCCTMLYLPFAEANTEAIOEQITRVLLERLIVNRPHPMGLITFIETI 2330
QY 193 KNPAKFMNHEFVHCAPBIEIKLFGSVAQCCMGOKAQOQVMEGTGAS 238
|||||
DB 2331 KNPAKFMNHEFVHCAPBIEIKLFGSVAQCCMGOKAQOQVMEGTGAS 2376

RESULT 7
US-10-491-566-72
; Sequence 72, Application US/10491566
; Publication No. US20040249144A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies Inc
; TITLE OF INVENTION: Regulated Breast Cancer Genes
; FILE REFERENCE: 3U 103 R1
; CURRENT APPLICATION NUMBER: US/10/491,566
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 2376
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-491-566-72

Query Match 94.8%; Score 1178; DB 16; Length 2376;
Best Local Similarity 99.6%; Pred. No. 3.4e-116;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLSRINIAPIRLTNFTGVPMPQPKDLDYLTKTRSPVTPLSDLRSLQVSNBGNRY 72
:|||||
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Db 2151 KYDMLSEINIAPIRLTNFTGVMPPOPKDLSYIKTRSPVTFPLSDLRSLQVSNBGNRY 2210
QY 73 NQOLINALVYVGTQALIAIHINKGSTPSMSTITHSAHMDIFQNLAVDLDTGGRYFLNAI 132
Db 2211 NQOLINALVYVGTQALIAIHINKGSTPSMSTITHSAHMDIFQNLAVDLDTGGRYFLNAI 2270
QY 133 ANQLRYPNSHTYFSCMTLYLPAEANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 192
Db 2271 ANQLRYPNSHTYFSCMTLYLPAEANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 2330
QY 193 KNPAPKFNHHEFVHCAPETIEKLFQSYAOCCKGQKQAQVMEGTGA 238
Db 2331 KNPAPKFNHHEFVHCAPETIEKLFQSYAOCCKGQKQAQVMEGTGA 2376

RESULT 8

US-10-369-493-5760
Sequence 5760, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5760
LENGTH: 2500
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-369-493-5760

Query Match 52.5%; Score 653; DB 15; Length 2500;
Best Local Similarity 53.8%; Pred. No. 7, 5e-60;
Matches 121; Conservative 34; Mismatches 70; Indels 0; Gaps 0;
QY 13 QVDMLESEINIAPIRLTNFTGVMPPOPKDLSYIKTRSPVTFPLSDLRSLQVSNBGNRY 72
Db 2256 QVDTLPEKAVBEKSNINAMTITIPDNIRILDEYLANRISVDLPILPITLQONQAGTGY 2315
QY 73 NQOLINALVYVGTQALIAIHINKGSTPSMSTITHSAHMDIFQNLAVDLDTGGRYFLNAI 132
Db 2316 NQOLINALVYVGTQALIAIHINKGSTPSMSTITHSAHMDIFQNLAVDLDTGGRYFLNAI 2375
QY 133 ANQLRYPNSHTYFSCMTLYLPAEANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 192
Db 2376 ANQLRYPNSHTYFSCMTLYLPAEANTBAIOEQITRVLLERLIYNRPHPWGLITFIELI 2435
QY 193 KNPAPKFNHHEFVHCAPETIEKLFQSYAOCCKGQKQAQVMEGTGA 237
Db 2436 KNPAPKFNHHEFVHCAPETIEKLFQSYAOCCKGQKQAQVMEGTGA 2480

RESULT 9

US-10-424-599-180820
Sequence 180820, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180820
; LENGTH: 394
; TYPE: PRT
; ORGANISM: glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134295C.1.pep
US-10-424-599-180820

Query Match 52.2%; Score 648.5; DB 15; Length 394;
Best Local Similarity 60.1%; Pred. No. 1.7e-60;
Matches 140; Conservative 23; Mismatches 49; Indels 21; Gaps 7;

QY 17 LSEINIAPIRLTNFTGVMPPOPKDLSYIKTRSPVTFPLSDLRSLQVSNBGNRY 68
Db 161 LRETTQSPRLSEVDAAKAKOMKVDBEYLKTRQSSP--FLSELKOKLISPEEASA 218
QY 69 GNRVNLQINALVYVGTQALIAIHINKGSTPSMSTITHSAHMDIFQNLAVDLDTGGRYFLNAI 119
Db 219 GNRVNLQINALVYVGTQALIAIHINKGSTPSMSTITHSAHMDIFQNLAVDLDTGGRYFLNAI 276
QY 120 LDTGGRYFLNAINANQLRYPNSHTYFSCMTLYLPAEANTBAIOEQITRVLLERLIYNRP 179
Db 277 LDTGGRYFLNAINANQLRYPNSHTYFSCMTLYLPAEANTBAIOEQITRVLLERLIYNRP 336
QY 180 HPWGLITFIELIKNPAPKFNHHEFVHCAPETIEKLFQSYAOCCKGQKQAQVMEGTGA 232
Db 337 HPWGLITFIELIKNPAPKFNHHEFVHCAPETIEKLFQSYAOCCKGQKQAQVMEGTGA 389

RESULT 10

US-10-425-114-59023
Sequence 59023, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59023
LENGTH: 683
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700096523_F1.1.pep
US-10-425-114-59023

Query Match 51.6%; Score 641; DB 15; Length 683;
Best Local Similarity 57.1%; Pred. No. 2.3e-59;
Matches 136; Conservative 27; Mismatches 55; Indels 20; Gaps 6;

QY 13 QVDMLESEINIAPIRLTNFTGVMPPOPKDLSYIKTRSPVTFPLSDLRSLQVSNBGNRY 67
Db 442 KIDDLAETSIAPRIMSVDGALKSKQKTEVDEYIKRPEGSSFLSDNQLKLLQONBASFV 501
QY 68 PGNRYNLQINALVYVGTQALIAIHINKGSTPSMSTITHSAHMDIFQNLAVDLDTGGRYFLNAI 116
Db 502 AGRYVNLQINALVYVGTQALIAIHINKGSTPSMSTITHSAHMDIFQNLAVDLDTGGRYFLNAI 561
QY 117 AVDLDTGGRYFLNAINANQLRYPNSHTYFSCMTLYLPAEANTBAIOEQITRVLLERLIYNRP 176
Db 562 ITSDTBERYFLNAINANQLRYPNSHTYFSCMTLYLPAEANTBAIOEQITRVLLERLIYNRP 621
QY 177 NRPHPWGLITFIELIKNPAPKFNHHEFVHCAPETIEKLFQSYAOCCKGQKQAQVMEGTGA 234

```

1 TYPE: PRT
2 ORGANISM: Zea mays
3 PRATURE:
4 OTHER INFORMATION: Clone ID: MRT4577_106800C.1.pdf
5 US-10-425-115-192123

```

APPLICANT: La Roba, Th

APPLICANT: La Roba, Th

[illegible]

Search completed: July 14, 2005, 20:37:44
Job time : 74.2171 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 14, 2005, 20:14:28 ; Search time 16.3411 Seconds

(without alignments)
1401.351 Million cell updates/sec

Title: US-10-019-151C-1

Perfect score: 1243
Sequence: 1 MILLVILAFILMGVDMSEI.....AGCCMGKQAQVMEGTGAS 238

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	94.8	1100	T17270	hypothetical prote
2	653	52.5	2500	G88493	protein F57B9.2 [1
3	615.5	49.5	1865	G88152	T1723.15 protein -
4	317	25.5	2100	T38128	CT123.15 protein -
5	231.5	18.6	2108	S28417	CDC39 protein - ye
6	95.5	7.7	2819	A90551	conserved hypochet
7	90	7.2	240	B64461	hypothetical prote
8	86	6.9	251	F89929	hypothetical prote
9	86	6.8	414	G89862	NAD-specific gluta
10	84.5	6.8	1125	S67794	probable membrane
11	83.5	6.7	378	E59094	hypothetical prote
12	83.5	6.7	378	T25176	hypothetical prote
13	83	6.7	350	AH3020	conserved hypochet
14	83	6.7	350	A98264	hypothetical 33.7k
15	82.5	6.6	428	H96641	hypothetical prote
16	82.5	6.6	536	S15183	gas-vesticle operon
17	82.5	6.6	536	T08241	gas-vesticle operon
18	82.5	6.6	781	T18693	gas-vesticle prote
19	82	6.6	733	T03117	glycoprotein H - a
20	81.5	6.6	536	G88954	protein K04P1.13 [
21	81.5	6.6	1039	B71342	hypothetical prote
22	81	6.5	263	T16339	hypothetical prote
23	81	6.5	312	F64435	mevalonate kinase
24	80.5	6.5	411	AD1342	ABC transporter (m
25	80	6.4	367	T139649	lipoprotein - Acti
26	80	6.4	658	H90013	hypothetical prote
27	79.5	6.4	636	T26993	hypothetical prote
28	79.5	6.4	552	J01788	DNA ligase (ATP) (
29	79.5	6.4	552	WNVZ7W	DNA ligase (ATP) (

30	79.5	6.4	1034	2	A82563	acetylflavin resista
31	79.5	6.4	1799	2	AD1895	serine/threonine k
32	79.5	6.4	2332	1	GNNTR	genome polypoteine
33	79	6.4	354	2	C89860	hypothetical prote
34	79	6.4	492	2	C84142	hypothetical prote
35	79	6.4	560	2	S29307	poly(3-hydroxyalka
36	79	6.4	638	2	B34285	NADH2 dehydrogenas
37	79	6.4	830	2	S55940	factor arrest prot
38	79	6.4	1015	2	B84458	probable retrovira
39	78.5	6.3	376	2	A44940	actin - pork tapew
40	78.5	6.3	890	1	J01947	genome polypoteine
41	78	6.3	462	2	S10439	DNA-directed RNA p
42	78	6.3	529	2	B84813	hypothetical prote
43	78	6.3	558	1	MMXRT	RNA 10 protein - r
44	78	6.3	575	2	S72283	DNA-directed RNA p
45	78	6.3	700	2	B69146	sensory transducti

ALIGNMENTS

RESULT 1

T17270
hypothetical protein DKFP434N241.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T17270

R/Poussacka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A/Reference number: Z18723

A/Accession: T17270

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-1100 <POU>

A/Cross-references: UNIPROT:Q9UPR8; EMBL:AL117492

A/Experimental source: adult testis; clone DKFP434N241

A/Genetics:

A/Note: DKFP434N241.1

Query Match 94.8%; Score 1178; DB 2; Length 1100;
Best Local Similarity 99.6%; Pred. No. 5.1e-97;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	13	QVMSBINIAPILINFTGVPMPORFKDLSYLRSPYTPISDLSNLOVNEPGRY 72
DB	875	KVMSBINIAPILINFTGVPMPORFKDLSYLRSPYTPISDLSNLOVNEPGRY 934
QY	73	NLQINLVLYVGTQIAIHNNKSTPMSSTTHSAHMDIFQMLAVDLDTGRTLPINAI 132
DB	935	NLQINLVLYVGTQIAIHNNKSTPMSSTTHSAHMDIFQMLAVDLDTGRTLPINAI 994
QY	133	ANQLRPNSTHTFSCMTLYLFAEANTTAIOEOITVLERLIVNRPWGLITPTELI 192
DB	995	ANQLRPNSTHTFSCMTLYLFAEANTTAIOEOITVLERLIVNRPWGLITPTELI 1054
QY	193	KNDAPFVWNEFVHCAPETIKLFQSYAQCCKGKQAQVMEGTGAS 238
DB	1055	KNDAPFVWNEFVHCAPETIKLFQSYAQCCKGKQAQVMEGTGAS 1100
RESULT 2		
G88493		
protein F57B9.2 [imported] - Caenorhabditis elegans		
C:Species: Caenorhabditis elegans		
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004		
C/Accession: G88493		
R/Anonymous, The C. elegans Sequencing Consortium.		
Science 282, 2012-2018, 1998		
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo		
A/Reference number: A75000; WUID:99069613; PMID:9851916		
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.el		
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; am		
A/Accession: G88493		

A:Reference number: S19415
A:Accession: S19770
A:Molecule type: DNA
A:Residues: 1852-2107 <LIN>
A:Cross-references: EMBL:X59720; MIPS:YCR093w
C:Genetics:
A:Gene: SGD: CDC3
A:Cross-references: SGD: S0000689; MIPS: YCR093w
A:Map position: 3R
C:Keywords: nucleus; transcription regulation; transmembrane protein
F:22-38/Domain: transmembrane #status predicted <TM1>
F:269-285/Domain: transmembrane #status predicted <TM2>
F:342-358/Domain: transmembrane #status predicted <TM3>
F:366-402/Domain: transmembrane #status predicted <TM4>
F:562-578/Domain: transmembrane #status predicted <TM5>
F:663-680/Domain: transmembrane #status predicted <TM6>
F:785-801/Domain: transmembrane #status predicted <TM7>
F:842-858/Domain: transmembrane #status predicted <TM8>
F:1439-1455/Domain: transmembrane #status predicted <TM9>
F:1635-1656/Domain: transmembrane #status predicted <TM10>
F:1665-1681/Domain: transmembrane #status predicted <TM11>
F:1751-1767/Domain: transmembrane #status predicted <TM12>
F:1773-1789/Domain: transmembrane #status predicted <TM13>
F:1801-1817/Domain: transmembrane #status predicted <TM14>
F:1928-1944/Domain: transmembrane #status predicted <TM15>

Query Match 18.6%; Score 231.5; DB 2; Length 2108;
Best Local Similarity 32.6%; Pred. No. 5.4e-12;
Matches 63; Conservative 40; Mismatches 77; Indels 13; Gaps 6;

39 KQDLSYTKRSPV---TPISDL-RSNLQVNEBGRNY---NLQINLVVYGTQAIH 91
1890 KRPVDNLRIPSNLSLTIISAIKDYTDIKGQVGFPLSDSKLPAIVLWGI--AG 1947
Db
92 IHNGSTPSNSTITHSAMDFQMLAVDLDTGRTFLMANQLRYPNSHTHYFSCMTL 151
1948 IEXKRTSNVAVPTKSSYYTLFPLIQNGSIEMKYQIILSVEDLRYPNHTWFSFLM 2007
Db
152 YLPA--EANT--AIQGITRVLLERLIVNRPFWGLITFELIKPAKFNHAEVHC 207
2008 NMFKSDPMNDQKLEVOEIIILNPLKRIIVNKPHTGVSVFPTQIINNNDINLDPVQS 2067
Db
208 APRIEKLFQSVAQ 220
2068 VPEIKLILQQLVK 2080
Db

RESULT 6
A90551
conserved hypothetical protein MYPU_3130 [imported] - Mycoplasma pulmonis (strain UAB CT
C/Species: Mycoplasma pulmonis
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: A90551
R:Chamblaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallsen, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A9512; MUID:21267165; PMID:11353084
A:Accession: A90551
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-2819 <NR>
A:Cross-references: UNIPROT:Q98Q98; GB:AL445566; PID:G14089727; PIDN:CAIC13486.1; GSPDB:G
C/Genetics:
A:Experimental source: strain UAB CT1P
A:Gene: MYPU_3130
A:Genetic code: SGCS

Query Match 7.7%; Score 95.5; DB 2; Length 2819;
Best Local Similarity 25.2%; Pred. No. 12;
Matches 62; Conservative 33; Mismatches 86; Indels 65; Gaps 12;

14 VDMLEINIAPIRLITNFTGVMP---PQPK-KDLSYTK--TRSPVTLSD-----L 58

Db
2056 IDALSTNIYEKLEVFLEAVKQKQNPSTKNDLFASTQELIKSPFQSGNGLPVLSIIL 2115
59 RSNLQVNEBGRNYTLQINLV-----LYGTQAIHAI-----HNK----- 95
Db
2116 KSNILDSKSIINKEVYQKVTLEFKLKNTSVQFVXDKTEINISKSIPLEQNNKQSLSK 2175
96 -----GSTPSMSTITHSAMDFPON-----LAVDLDTESRY--FLNATANQ 135
Db
2176 IVALIASDPQTTMLVNVKVIDIDIFQNHKNVASKANLNLBFLTHKQQLAYLSKSTNK 2235
Qy
136 LRYNSHTHYFSCMTL--YLFAANT--AIQGITRVLL--RLIVNRPFWGLITF 188
Db
2236 LNVKVSLEHDFSVNVLLSQLSKQNIIFNNKEKQSLKSTIKTSIHLINDIPQLVNLN 2295
Qy
189 TELIKN 194
Db
2296 IEEIKN 2301

RESULT 7
B64461
hypothetical protein MJ1291 - Methanococcus jannaschii
C/Species: Methanococcus jannaschii
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 04-Mar-2000
C/Accession: B64461
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
R.; Reich, C.I.; Overbeek, R.; Klier, B.F.; Weierbeck, K.G.; Merrick, J.M.; Glodex, A.
rson, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klek, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: B64461
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-240 <BUL>
A:Cross-references: GB:U67569; GB:L77117; NID:G1591918; PID:G1591928; TIGR: MJ1291; PID:
C/Genetics:
A:Map position: REV1238450-1237728
C:Superfamily: Methanococcus jannaschii hypothetical protein MJ1291

Query Match 7.2%; Score 90; DB 2; Length 240;
Best Local Similarity 21.7%; Pred. No. 1.4;
Matches 47; Conservative 37; Mismatches 83; Indels 50; Gaps 9;

3 LVLTLAFLYLMQVMLSEI--NIAPRLITNFTGVMPQPKDLSYTKRSPVFLSDRS 60
Db
20 IVTGAAYVAMSNKVPFDTTEKIRPTIKSSIGNIKPIBISTIEYFTN-----LDLNG 73
Qy
61 NLOVNEBGRNYLQINLVLYVGTQAIHINHGKS-----TPSMSTITHSAH 109
Db
74 DSRITNPPERR-----FIQTIKXFINNIDBDLNKXNRIYCLTFNVWASVNIID 122
Qy
110 MDLFOMLAVDLDT-----BGRYVFLNAINQLRYPNSHTHYFSCMTLYLFAANTEAIOE 164
Db
123 -DSSNNLLDRDENPNTYSSQIVYFNGTV---YYSMKFYDENGKLFYAAASNGNMLN- 176
Qy
165 QITRVLLERLIVNRPFWGL-----ITFELIKN 194
Db
177 --TSNLLDLIDNCPFBSPFLKNGSKTIDINYIILNN 211

RESULT 8
F89929
hypothetical protein SA133 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: F89929
R:Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu-
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

Best Local Similarity 21.9%; Pred. No. 9.6;
Matches 51; Conservative 36; Mismatches 72; Indels 74; Gaps 12;

```

QY 26 ILTNPTGV--MPPQFKDLD---SYLKTSF-----VTFISLDRSNLQVSNRPGRNYNLQ 75
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 20 ILVLFAGIKIVPGHRYVERFGRYRTLEPGNLIIPEPESIGSKNNVMEQ----- 71
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 76 LINALVLYGTQAIHAIHNKGSTPSMSTTHSAHMDIFQNLAVDLDTBGRYLFNLAIANQ 135
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 72 ----VHIIPTQEV-----ITR-----DNASVSDAVTFYQVLNAAQAA 105
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 136 LRYNSHTHYFSCITMLYLPAA-----ANTEAIOEQITRVLRLIYNRPHPGILL 185
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 106 YQISNQLQMAIENLTMTNINSVWGSMDELDSNRDAINDRLAVNDEAV-----GPMGIK 160
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 186 ITFIELIKNPAPFKFNNHEFVHCAPETIKLFQSVAGCCMGOKAQ-QVMEGTGA 237
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 161 VTRIE-IKD-----IAP-KDVLDSMARQMKAREKRAQVLEAEGA 199
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 15

H96641
hypothetical protein T25B24.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96641
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
C.A.; Li, J.H.; Li, Y.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Authors: Hunter, J.L.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maltf, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96641
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <STO>
A:Cross-references: UNIPROT:Q9SY86; GB:AB005173; NID:94585871; PIDN:AAD25544.1; GSPDB:GN
C:Genetics:
A:Gene: T25B24.1
A:Map position: 1

Query Match 6.6%; Score 82.5; DB 2; Length 428;

Best Local Similarity 21.2%; Pred. No. 14;

Matches 48; Conservative 33; Mismatches 104; Indels 41; Gaps 9;

```

QY 9 FYIMQVDMLESEINARILILNPTGVMPPQFKDLDSTYKTRSPVTFISLDRSNLQVSNRP 68
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 167 YMLSQVDLSREASHLSRFYTFNFGWQVSPKPIYPLI--HPAVLVETYEHEGSVARYV 223
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 69 GNRYNQLINALVLYGTQAIHAIHNKGSTPSMSTTHSAHMDIFQ-NLAVDLDTBGRYL 127
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 224 DSGEGEKAKAKAHGIGNALL-----KLLVDNFTHADMPGNIIIVRNNTRRGL 274
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 128 PLNALINQLRYNSHTHYFSCITMLYLPAAANTE-----AIOEQITRVLRLI----- 175
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 275 F-----RSRKHIVFLDVGTAEISKTRDNLGFPAVARRDGRTAERTLKLKSKQ 326
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 176 VNRHPHMGILLITFIELIKNPAPFKFNNHE--FVHCAPETIKLFQSV 218
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 327 QNCPDPO---AFIKVEER-AFTFGTBEGLVHPADCMHELPERKM 367
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: July 14, 2005, 20:33:08
Job time : 23.3411 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:55:46 ; Search time 74.5891 Seconds
(without alignments)
1633.949 Million cell updates/sec

Title: US-10-019-151C-1

Perfect score: 1243
Sequence: 1 MILLVILAFYLMQVDMLESI.....AGCCMGQKQKQVMEGTGAS 238

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	94.8	539	2	Q9BVZ6
2	1178	94.8	1100	2	Q9URR8
3	1178	94.8	1117	2	Q8K3D8
4	1178	94.8	1458	2	Q6Z008
5	1178	94.8	1620	2	Q8T5B3
6	1178	94.8	1835	2	Q9Y2I0
7	1178	94.8	2137	2	Q68DX7
8	1171	94.2	381	2	Q8C0H2
9	905.5	70.2	1872	2	Q7PW82
10	873	70.2	669	2	Q8IH39
11	873	70.2	2170	2	Q9V591
12	873	70.2	2172	2	Q8MKU3
13	794	63.9	424	2	Q8BX82
14	653	52.5	2500	2	Q20937
15	621.5	50.0	2363	2	Q94LQ9
16	615.5	49.5	682	2	Q84W89
17	615.5	49.5	1865	2	Q81909
18	604.5	48.6	2526	2	Q75JL4
19	603	48.5	316	2	Q9UJ27
20	506.5	40.7	3371	2	Q81TW4
21	467.5	37.6	2589	2	Q7Y1T7
22	439	35.3	2145	2	Q675U0
23	439	35.3	4466	2	Q81LS4
24	389.5	31.3	2017	2	Q6C0P0
25	381.5	30.7	463	2	Q7BM05
26	342	27.5	2223	2	Q6BQK3
27	323.5	26.0	947	2	Q7RK48
28	317	25.5	2100	2	P87112
29	270.5	21.8	1400	2	Q9N9L6
30	268.5	21.6	581	2	Q95T66
31	256	20.6	2098	2	Q7S687

32	252	20.3	2141	2	Q75DB4	Q75DB4	aehya_goss
33	249	20.0	2140	2	Q6CSR0	Q6CSR0	kluyveromyc
34	231.5	18.6	2108	1	NOT1_YEAST	P25655	saccharomyc
35	215.5	17.3	2090	2	Q6TVN7	Q6TVN7	candida_gla
36	107	8.6	1049	2	Q6TVY2	Q6TVY2	debaromyce
37	97	7.8	524	2	Q6BVH7	Q6BVH7	candida_gla
38	96	7.7	240	1	YC91_MERJA	Q6CVJ3	methanococc
39	96	7.7	441	2	Q6CVJ3	Q6CVJ3	kluyveromyc
40	95.5	7.7	2819	2	Q980P8	Q980P8	mycoplasma
41	94.5	7.6	560	2	Q939A6	Q939A6	pseudomonas
42	94.5	7.6	1264	2	Q9ACB4	Q9ACB4	pseudomonas
43	94.5	7.6	43	2	Q7RPM6	Q7RPM6	plasmidium
44	93.5	7.5	473	1	SYC_METAC	Q8EP6	methanosarc
45	92.5	7.4	355	2	Q8EH8	Q8EH8	shewanella

ALIGNMENTS

RESULT 1
Q9BVZ6 PRELIMINARY; PRT; 539 AA.
ID Q9BVZ6
AC Q9BVZ6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE KIAA1007 protein (Fragment).
GN Name=KIAA1007;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Pelngold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
RA Sapelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RT Jones S.J., Marra M.A.;
RT "denaturation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX Strausberg R.;
RL Submitted (NCV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC000779; AAH00779.2; -;
DR InterPro; IPR001220; Lectin_legb.
DR Pfam; PF04054; Ncrl; 1.
DR PROSITE; PS00307; LECTIN_LEGUMB_BETA; UNKNOWN_1.
FT NON_TER 1 1
SQ
SEQUENCE 539 AA; 61829 MW; E59AB5187B1BDF5 CRC64;
Query Match 94.8%; Score 1178; DB 2; Length 539;
Best Local Similarity 99.6%; Pred. No. 3, 7e-94;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 13 QVDMLESEINAPRIILNFTGVPMPQPKDLSYLKTRSPVTFPLSDLRSMLOVSNBPGNRY 72
DB 314 KYDMLESEINAPRIILNFTGVPMPQPKDLSYLKTRSPVTFPLSDLRSMLOVSNBPGNRY 373
QY 73 NIQLINALVLYVGTOAIAIHINKGSTPMSSTITHSAMDIFONLAVDLDTGGRYFLNMI 132
DB 374 NIQLINALVLYVGTOAIAIHINKGSTPMSSTITHSAMDIFONLAVDLDTGGRYFLNMI 433
QY 133 ANQLRYPNSHTYFSCMTLYLFAEANTAEALQEQITRVLLERLIVNRPHPGILLITFIELI 192
DB 434 ANQLRYPNSHTYFSCMTLYLFAEANTAEALQEQITRVLLERLIVNRPHPGILLITFIELI 493
QY 193 KNPAKFMNHEFVHCAPETIEKLFQSVAAQCCMGOKQAQVMEGTGAS 238
DB 494 KNPAKFMNHEFVHCAPETIEKLFQSVAAQCCMGOKQAQVMEGTGAS 539

RESULT 2
QJUPR8 ID QJUPR8 PRELIMINARY; PRT; 1100 AA.
AC QJUPR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFp434N241 (Fragment).
GN Name=DKFp434N241;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117492; CAB55960.1; -.
DR PIR; T17270; T17270.
DR InterPro; IPR001220; Lectin_legb.
DR InterPro; IPR007196; Noct1.
DR Pfam; PF04054; Noct1; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 1100 AA; 124718 MW; 046DA23BD314A46F CRC64;

Query Match 94.8%; Score 1178; DB 2; Length 1100;
Best Local Similarity 99.6%; Pred. No. 8.8e-94;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DE RIKEN cDNA 603041IK04.
GN Name=603041IK04Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018281; AAH18281.1; -.
DR MGD; MG1:2442402; 603041IK04Rik.
DR InterPro; IPR001220; Lectin_legb.
DR InterPro; IPR007196; Noct1.
DR Pfam; PF04054; Noct1; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
SQ SEQUENCE 1117 AA; 126687 MW; 49AD7FF80D449D97 CRC64;

Query Match 94.8%; Score 1178; DB 2; Length 1117;
Best Local Similarity 99.6%; Pred. No. 9e-94;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
Q8K3D8 ID Q8K3D8 PRELIMINARY; PRT; 1117 AA.
AC Q8K3D8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
RESULT 4
Q6ZQ08 ID Q6ZQ08 PRELIMINARY; PRT; 1458 AA.
AC Q6ZQ08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE KIAA1007 protein (Fragment).
```


OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic tail;
 RX PubMed=14621295;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
 Saga Y., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIA gene:
 RT III. the complete nucleotide sequences of 500 mouse KIA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:167-180(2003).
 DR EMBL: AK129258; BAC98068.2; -;
 DR Interpro: IPR001220; Lectin_legB.
 DR Pfam: PF04054; Noct1; 1.
 DR PROSITE: PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
 FT NON TER 1 1
 SQ SEQUENCE 1458 AA; 165136 MW; 7752261AAA0BAFC9 CRC64;
 Query Match 94.8%; Score 1178; DB 2; Length 1458;
 Best Local Similarity 99.6%; Pred. No. 1.2e-93;
 Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QVDMLESEINIAPIRLNFTGWPMPQPKOLDSTLKRSPVTLSDLSNLOVSEBGNRY 72
 DB 1233 KVDMLSEINIAPIRLNFTGWPMPQPKOLDSTLKRSPVTLSDLSNLOVSEBGNRY 1292
 QY 73 NQOLINALVYGTQAIHAIHNKGSTPSMSTITHSAMMDI FQNLAVDLDTGEGYFLPNAI 132
 DB 1293 NQOLINALVYGTQAIHAIHNKGSTPSMSTITHSAMMDI FQNLAVDLDTGEGYFLPNAI 1352
 QY 133 ANQLRPNSHTHYFSCITMLYLPABANTBAIQEQITVLLERLLVNRPHPGLLITFIELI 192
 DB 1353 ANQLRPNSHTHYFSCITMLYLPABANTBAIQEQITVLLERLLVNRPHPGLLITFIELI 1412
 QY 193 KNPAPFKNHBFVHCAPBEIKL FQSVACCCMGKQKQAOVMEGTGAS 238
 DB 1413 KNPAPFKNHBFVHCAPBEIKL FQSVACCCMGKQKQAOVMEGTGAS 1458

RESULT 5
 Q8TB53 PRELIMINARY; PRT; 1620 AA.
 AC Q8TB53;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE KIAA1007 protein (Fragment).
 GN Name=KIAA1007;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ueda N.B., Toshikiyoki S., Canninci P., Prange C.,
 Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 Villalón D.K., Muzny D.M., Sodergren J., Lu X., Gibbs R.A.,
 Fehey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green R.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Kravitz M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC024317; AAH24317.1; -;
 DR Interpro: IPR001220; Lectin_legB.
 DR Pfam: PF04054; Noct1; 1.
 DR PROSITE: PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
 FT NON TER 1 1
 SQ SEQUENCE 1620 AA; 183241 MW; 6F59D887182E0A63 CRC64;
 Query Match 94.8%; Score 1178; DB 2; Length 1620;
 Best Local Similarity 99.6%; Pred. No. 1.4e-93;
 Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 13 QVDMLESEINIAPIRLNFTGWPMPQPKOLDSTLKRSPVTLSDLSNLOVSEBGNRY 72
 DB 1395 KVDMLSEINIAPIRLNFTGWPMPQPKOLDSTLKRSPVTLSDLSNLOVSEBGNRY 1454
 QY 73 NQOLINALVYGTQAIHAIHNKGSTPSMSTITHSAMMDI FQNLAVDLDTGEGYFLPNAI 132
 DB 1455 NQOLINALVYGTQAIHAIHNKGSTPSMSTITHSAMMDI FQNLAVDLDTGEGYFLPNAI 1514
 QY 133 ANQLRPNSHTHYFSCITMLYLPABANTBAIQEQITVLLERLLVNRPHPGLLITFIELI 192
 DB 1515 ANQLRPNSHTHYFSCITMLYLPABANTBAIQEQITVLLERLLVNRPHPGLLITFIELI 1574
 QY 193 KNPAPFKNHBFVHCAPBEIKL FQSVACCCMGKQKQAOVMEGTGAS 238
 DB 1575 KNPAPFKNHBFVHCAPBEIKL FQSVACCCMGKQKQAOVMEGTGAS 1620

RESULT 6
 Q9Y2L0 PRELIMINARY; PRT; 1635 AA.
 AC Q9Y2L0;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE KIAA1007 protein (Fragment).
 GN Name=KIAA1007;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99246063; PubMed=10231032; Kikuno R., Hiraoka M.,
 Nagase T., Ishikawa K., Suyama M., Kikuno R., Ohara O.,
 Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:63-70(1999).
 DR EMBL: AB023224; BAA76851.2; -;
 DR Interpro: IPR001220; Lectin_legB.
 DR Pfam: PF04054; Noct1; 1.
 DR PROSITE: PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.
 FT NON TER 1 1
 SQ SEQUENCE 1835 AA; 206328 MW; BD9B12C857A71175 CRC64;

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Query Match          94.8%; Score 1178; DB 2; Length 1835;
Best Local Similarity 99.6%; Pred. No. 1.6e-93;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMSEINIARILNFTGVPMPQPKOLDYLKTRSPVTLSDLRSLQVSNPEGNRY 72
   :|||||
Db 1610 KYDMSSEINIARILNFTGVPMPQPKOLDYLKTRSPVTLSDLRSLQVSNPEGNRY 1669

QY 73 NQOLINALVYGTQAIHAIHNKSTPSSMTITSHAHMDIFQNLAVDLDTREGYFLNMI 132
   :|||||
Db 1670 NQOLINALVYGTQAIHAIHNKSTPSSMTITSHAHMDIFQNLAVDLDTREGYFLNMI 1729

QY 133 ANQLRYPNSHTYFSCITMLYFLPAEANTBAIOEQITRVLLERLIYNRPHPMGLITITIELI 192
   :|||||
Db 1730 ANQLRYPNSHTYFSCITMLYFLPAEANTBAIOEQITRVLLERLIYNRPHPMGLITITIELI 1789

QY 193 KNPAPKFMNHEFVHCAPETIEKLFQSVAAQCCMGKQAAQVMEGTGAS 238
   :|||||
Db 1790 KNPAPKFMNHEFVHCAPETIEKLFQSVAAQCCMGKQAAQVMEGTGAS 1835

RESULT 7
Q6BDX7 PRELIMINARY; PRT; 2127 AA.
ID Q6BDX7;
AC Q6BDX7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686B0722.
GN Name=DKFZp686B0722;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RG The German CDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schnupp I., Wellenreuther R.,
RA Mewes H.W., Weill B., Amd C., Oesinger A., Fobo G., Han M., Wiemann S.;
RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749237; CNI18093.1;
DR InterPro; IPR001220; Lectin_legB.
DR InterPro; IPR007196; Lectin_legB.
DR Pfam; PF04054; Noct1; 1.
DR PROSITE; PS00307; LECTIN_LBGIME_BETA; UNKNOWN_1.
SQ SEQUENCE 2127 AA; 239113 MW; ABSDI992D6944037 CRC64;

Query Match          94.8%; Score 1178; DB 2; Length 2127;
Best Local Similarity 99.6%; Pred. No. 2e-93;
Matches 225; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMSEINIARILNFTGVPMPQPKOLDYLKTRSPVTLSDLRSLQVSNPEGNRY 72
   :|||||
Db 1902 KYDMSSEINIARILNFTGVPMPQPKOLDYLKTRSPVTLSDLRSLQVSNPEGNRY 1961

QY 73 NQOLINALVYGTQAIHAIHNKSTPSSMTITSHAHMDIFQNLAVDLDTREGYFLNMI 132
   :|||||
Db 1962 NQOLINALVYGTQAIHAIHNKSTPSSMTITSHAHMDIFQNLAVDLDTREGYFLNMI 2021

QY 133 ANQLRYPNSHTYFSCITMLYFLPAEANTBAIOEQITRVLLERLIYNRPHPMGLITITIELI 192
   :|||||
Db 2022 ANQLRYPNSHTYFSCITMLYFLPAEANTBAIOEQITRVLLERLIYNRPHPMGLITITIELI 2081

QY 193 KNPAPKFMNHEFVHCAPETIEKLFQSVAAQCCMGKQAAQVMEGTGAS 238
   :|||||
Db 2082 KNPAPKFMNHEFVHCAPETIEKLFQSVAAQCCMGKQAAQVMEGTGAS 2127

RESULT 8
Q8COH2 PRELIMINARY; PRT; 381 AA.
ID Q8COH2
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AC Q8COH2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DE enriched library, clone:6030411K04 product:ADRENAL GLAND PROTEIN AD-
DE 005 homolog.
GN Name=6030411K04R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komno H., Akiyama J., Nishi K., Kitsuwa T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiroka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata H., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito P., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AK031357; BAC27364.1; -.
```

DR MGP;MGI:24432402; 60304411IK04RLK.
DR InterPro; IPR001220; Lectin_legB.
DR InterPro; IPR007196; NcL1______.
DR Pfam; PF040544; NcL1_1.
DR PROSITE; PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
SQ SEQUENCE 381 AA; 43877 MW; 2A1AC9P65AC87A52 CRC64

Query Match	94.2%	Score 1171	DB 2	Length 381
Best Local Similarity	99.1%	Pred. No. 1e-93		
Matches 221; Conservative	1	Mismatches	1	Indels 0; Gaps 0

QY	13	QYDMLSEINIAIRILITNFGVMPPOPKOLDSYLTQTSVPTE.SLRSLQVSNBGRNY	72
Db	156	KYDMLSEINIAIRILITNFGVMPPOPKOLDSYLTQTSVPTE.SLRSLQVSNBGRNY	215
QY	73	NIQLINALVLYVGTOAIAHINHKGSTPSMSTITTHSAHNDIFONTAVDLDTEGRY.FLNAI	132
Db	216	NIQLINALVLYVGTOAIAHINHKGSTPSMSTITTHSAHNDIFONTAVDLDTEGRY.FLNAI	275
QY	133	ANQLAFYNSHTHYFESCTMLYLPFAKANTBAIOEQITRVLLERLIIVRPHWGILLTFIETI	192
Db	276	ANQLAFYNSHTHYFESCTMLYLPFAKANTBAIOEQITRVLLERLIIVRPHWGILLTFIETI	335
QY	193	KNPA.FKFWNHBFVHCABRIETKL.FQSVAAOCMGQKAAQVMEETGAS	238
Db	336	KNPA.FKFWNHBFVHCABRIETKL.FQSVAAOCMGQKAAQVMEETGAS	381

RESULT 9	
Q7PW82	
ID Q7PW82	PRELIMINARY;
	PRT; 1872 AA

AC	Q7PWR82.1	01-MAR-2004	(TReMBLrel. 26, Created)
DT	01-MAR-2004	(TReMBLrel. 26, Last sequence update)	
DT	01-MAR-2004	(TReMBLrel. 26, Last annotation update)	
DE	ENSANGP00000016536 (Fragment).		
GN	Name=ENSANG00000014047;		
OS	Anopheles gambiae str. PEST.		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.		
OX	NCBI_TaxID=180454;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=PEST;		
RA	Anopheles Genome Sequencing Consortium;		
RL	Submitted (APR-2003) to the EMBL/Genbank/DBJ databases.		
CC	-1- CAUTION: The sequence shown here is derived from an		
CC	EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL; AAA001008984; EAA14758.1; -		
DR	InterPro; IPR001220; Lectin_legB.		
DR	InterPro; IPR007196; Nc1.		
DR	Pfam; PF04054; Nc1.1.		
DR	PROSITE; PS00307; LECTIN_LEGUMB_BETA; UNKNOWN_1.		
FT	NON_TER		
SQ	SEQUENCE	1872 AA; 211895 MW; 1DEBD36FAF028B1A CRC64;	

Query Match	72.8%	Score 905.5	DB 2	Length 1872
Best Local Similarity	77.0%	Pred. No. 9.7e-70		
Matches 171	Conservative 27	Mismatches 23	Indels 1	Gaps 1

[illegible]

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Qy      192 IKNPAFKFWNHRBFVHCAPBIEKLFSQVAOCMGKOAOQWME    233  
        ||| :||| :||||| :||| :||| :||| :  
Db     1821 IKNPITYKFWDHDFVHCAPBIERLFESVAKSCMVTSKSQOIQ   1862
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RESULT 10	
Q8IH39	
ID Q8IH39	PRELIMINARY;
DATE 08-07-69	PRT; 669 AA

AC 081439;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE GR26494P (Fragment).
GN ORFNames=CG1884;
OS Drosophila melanogaster (Pruit fly).
OC Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pearygota
OC Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
OC Ephydriodes, Drosophilidae, Drosophila.
OX NCBI_Taxid=7227;

Query Match	70.2%	Score 873;	DB 2;	Length 669;
Best Local Similarity	71.7%	Pred. No. 1,96-67;		
Matches 165; Conservative	30;	Mismatches 29;	Indels 6;	Gaps 2;

[illegible]

RESULT	11	
Q9V591		
ID	Q9V591	PRELIMINARY; PRT; 2170 AA.
AC	Q9V591;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-MAY-2004 (TREMBLrel. 26, Last annotation update)	
DE	CG1884 - PB.	
GN	ORFNames=CG1884;	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota	
NC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	

CC Ephydroidae, Drosophilidae; Drosophila.
OK NCBI TaxID=12277.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.H., Blazynski R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Bau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Berns P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottakov S.,
RA Butts K.C., Cawley S., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Chew J.S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo J.E., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodeon K., Doup L.E., Downes W., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dudbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischman W.,
RA Fowler C., Gabriellian A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA Golek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Housner K.A., Howland T.J., Wei M.H., Ibeagwu J.,
RA Jatala J.M., Kalush F., Karpen G.H., Ke Z., Kemson J.A., Kechum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberg C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusbaum D.R., Paclab U.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Put V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheefer P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Svirskas R., Spradling A.C., Stepieltom M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach U.,
RA Williams S.M., Woodagef, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426065; PubMed=12537568;
RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Fritze E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclab U.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stepieltom M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.B., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426070; PubMed=12537573;
RX Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Kaminler J.S., Fritze E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RN SEQUENCE FROM N.A.
RP MEDLINE=22426069; PubMed=12537572;
RX Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stepieltom M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

[illegible]

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup E.B., Downes W., Duncan-Rocha S., Dunkov B.C., Dunn P.,
RA Dudbin K.J., Evangelista C.C., Ferraz G., Ferreira S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heilmann T.T., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.U., Wei M.H., Idagham C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,
RA Kimmel B.B., Kodira C.D., Kreic C., Kravitz S., Kulip D., Lai Z.,
RA Liu X.P., Lei Y., Levitsky A.G., Li J., Li Z., Liang Y., Lin X.,
RA Luo X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mileshina N.V., Moberry C., Morris J., Mozhrefti A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,
RA Neilson D.R., Nelson K.A., Nixon K., Nusser-D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shie B.C., Sliden-Klamos I., Simpson M., Skupski M.F., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtak R., Teclor C., Turner R., Venner B., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.W., Weissbach J.,
RA Williams S.M., Woodgett G., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zavari J.S., Zhang M., Zhang G., Zhao O., Zheng L.,
RA Zhong X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RV
RW
RX SEQUENCE FROM N.A.
RY MEDLINE=22426065; PubMed=12537568;
RZ Celinker S.B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hokins R.A., Laverty T., Muray D.M., Nelson C.R.,
RA Paetel J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svrtakovsk G., Taborski P.E., Wan K., Stapperton M., Sutton G.G., Venner C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RL melanogaster euchromatic genome sequence.";
RM Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RQ MEDLINE=22426070; PubMed=12537573;
RX Kamlinher U.S., Bergman C.M., Kronmiller B., Carlson J., Svrtakovskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.B., Rubin G.M.,
RA Ashburner M., Celinker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* eu-chromatin:
RL a genomic perspective.";
RU Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RV SEQUENCE FROM N.A.
RW MEDLINE=22426069; Pubmed=12537572;
RX Maiba S., Crosby M.A., Munngill C.J., Matthews B.B., Campbell K.S.,
RA Hradscek P., Huang Y., Kaminkler U.S., Millburn G.H., Prochnik S.B.,
RA Smuth C.D., Tuhy J.L., Whittied E.J., Bayraktarglu L., Bernan B.P.,
RA Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stappleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.B.;
RT "Annotation of the *Drosophila melanogaster* eu-chromatic genome: a
RL systematic review.";
RM Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RV SEQUENCE FROM N.A.
RW Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.
RX Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RV SEQUENCE FROM N.A.
RW FlyBase;
RX Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
RZ EMBL; AB003833; AA071069_2; -
RA FlyBase; FBgn0033424; CGI884,
DR InterPro; IPRO00577; FGAT_Kln.
RR Interpro; IPRO003006; IG MEC.

Query Match

Best Local Similarity 70.2%; Score 873; DB 2; Length 2172;
Matches 165; Conservative 30; Mismatches 29; Indels 6; Gaps

Qy 13 QVDMSEINIAIRILTNF-TGVPMPQPKDLDSTYKTSPTFTSDDLASNLOVSNEGSR
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Dd 1936 KVDMLSDSSNAAPKVLSSTYMNIQPANPFKDLDSTYLAKARAPTFLSELGLHQLVTSEBCTR
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Qy 72 YNLQLNALVLVGQAIALHNKSSTSMSITSHASMDIFONLADLTDEGRYLPLANA
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Dd 1996 YNALLNNALVMYGVGTQDALLNKNKPFPPTSNTAISAMDFQNLAVALDTREGRYLPANA
||:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|

Qy 132 IANOATPYSNHHSCTWLYFAEANTEAIOEQITRVLRLIYNRPHPMGLITEIBL
||:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|
Dd 2056 INAQATPYPSHHYSCAVTLHFPAANESEAIOEQITRVLRLLIYNRHPPMGILLTIEBL
||:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|

Qy 192 IKNPAEFKPNHEPVHCAPRIETLVFSVAQCCKMKGAQQ-----VMBSTG 236
||:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|
Dd 2116 IKNPVKFDHDVFVCAPETITLFESVARSCIASKSVTVQALNMPEVDSGG 2165
||:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|:~::~|

RESULT 13

Q8BXB2 PRELMINARY; PRT; 424 AA.

AC OQBXB2;
BT 01-MAR-2003 (TrEMBLrel_23, Created)
DT 01-MAR-2003 (TrEMBLrel_23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel_26, Last annotation update)
Ds Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C13J0038P19 Product:ADRENAL GLAND PROTEIN AD-005 homolog.
DE Name=6030411K04RLk;
GN Mus musculus (Mouse);
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6j; TISSUE=Head;
RC MEDLINE=992919253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P.; Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6j; TISSUE=Head;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN Pantom Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6j; TISSUE=Head;
RC The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
RT Nature 420:563-573(2002).
[4]

SEQUENCE FROM N.A.
MEDLINE=C57BL/6j; TISSUE=Head;
CARDINAL=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komio H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to

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RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
  Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
  Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
  "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multicapillary sequencer.";
  Genome Res. 10:11757-11771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
  Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
  Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
  Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
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  Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
  Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
  Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
  Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
  Tagawa A., Takahashi F., Takaku-Akahita S., Takeda Y., Tanaka T.,
  Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK048177; BAC33267.1; -.
DR MGD; MGI:2442402; 603041IK04Rik.
DR InterPro; IPR001220; Lectin_legB.
DR InterPro; IPR007196; Noct1.
DR Pfam; PF04054; Noct1.
DR PROSITE; PS00307; Lectin_LEGUME_BETA; UNKNOWN 1.
SQ SEQUENCE 424 AA; 48770 MW; 615A08FD6C1FE03 CRC64;

Query Match      63.9%; Score 794; DB 2; Length 424;
Best Local Similarity 98.7%; Pred.No.8.5e-61;
Matches 154; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 QVDMLESEINIAPIRLITNFTGVMPQPKKDLSDYLKTRSPVTFSLDRLSNLOVSNRPGRY 72
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 269 KIDMLSEINIAPIRLITNFTGVMPQPKKDLSDYLKTRSPVTFSLDRLSNLOVSNRPGRY 328

QY 73 NQLINALVLYVGTQAIHAIHNKGSTPSMSTITHSAHMDI FQNLAVDLDTGRYFLNAI 132
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 329 NQLINALVLYVGTQAIHAIHNKGSTPSMSTITHSAHMDI FQNLAVDLDTGRYFLNAI 388

QY 133 ANQLRYPNSHTYFSCCTMLYLFPAEANTEAIOEQITR 168
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 389 ANQLRYPNSHTYFSCCTMLYLFPAEANTEAIOEQITR 424

RESULT 14
Q20937 PRELIMINARY; PRT; 2500 AA.
AC Q20937;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Not-like (Yeast ccr4/not complex component) protein 1.
GN Name=ntc-1; ORFNames=F57B9.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCB1_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
```

```
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pavello A.;
RT "The sequence of C. elegans cosmid F57B9.";
  Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
  Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
  Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
  Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U13876; AA21168.1; -.
DR PIR; G88493; G88493.
DR WormBase; WBGene0003824; ntl-1.
DR WormPeP; F57B9.2; CB01337.
DR InterPro; IPR01547; Glyco_hydro_5.
DR InterPro; IPR007196; Noct1.
DR Pfam; PF04054; Noct1.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN 1.
SQ SEQUENCE 2500 AA; 27890 MW; 055808606FF56975 CRC64;

Query Match      52.5%; Score 653; DB 2; Length 2500;
Best Local Similarity 53.8%; Pred.No.1.4e-47;
Matches 121; Conservative 34; Mismatches 70; Indels 0; Gaps 0;

QY 13 QVDMLESEINIAPIRLITNFTGVMPQPKKDLSDYLKTRSPVTFSLDRLSNLOVSNRPGRY 72
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2256 QVDTTPENAVEKSNLNATITIPDNIRIPLDEYLNRSVDPPLPFTLQTONQAGTKY 2315

QY 73 NQLINALVLYVGTQAIHAIHNKGSTPSMSTITHSAHMDI FQNLAVDLDTGRYFLNAI 132
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2316 NTVVNAALVLYGIAIHAIHILHRLRQIRISTLNIAHSYNDIFQNLAIQDTBERYLLFNGI 2375

QY 133 ANQLRYPNSHTYFSCCTMLYLFPAEANTEAIOEQITRVLIERLI VNRPHPGALLITFIELI 192
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2376 ANQLRYPNAHTYFSCVFLYLFKNSNTNDTIQEQITRILFERLVALRPHPGALLITFIELI 2435

QY 193 KNPARKFMNHEFVHCAPRIEKLFGSVACCMGQKQAQVMESTGA 237
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2436 KNPYTFMRYEFTSCAPEIQRLFQNVANTCVPAQSQPQAPDGA 2480

RESULT 15
Q94LO9 PRELIMINARY; PRT; 2363 AA.
AC Q94LO9; Q7XC99;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transcription regulatory protein.
GN ORFNames=OSUNBA0010C11.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCB1_Taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buehl C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
```

RA Bremner M., Burgess S., Hance M., Shvartsbeyn M., Taitlin T.,
 RA Riggs F., Heiao J., Ziemann V., Blunt S., Pal G., Vanaken S.E.,
 RA Utechtack T.R., Feildilyum T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.,
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buell R.,
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RT The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 RT chromosome 10.";
 RL Science 300:1566-1569(2003).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Ming R.A., McComble W.R., Messing J., Yuan Q.,
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL/AC069300; AAK55455.1; -.
 DR EMBL/AB017118; AAP54975.1; -.
 DR Gramene; Q7XC99; -.
 DR Gramene; Q94LQ9; -.
 DR InterPro; IPR007196; Noct1.
 DR Pfam; PF04054; Noct1; 1.
 SO SEQUENCE 2363 AA; 262004 MW; 24B523628FCA875C CRC64;

Query Match 50.0%; Score 621.5; DB 2; Length 2363;
 Best Local Similarity 55.1%; Pred. No. 7.5e-45;
 Matches 125; Conservative 38; Mismatches 49; Indels 15; Gaps 5;

QY 13 QVMDLSHINIAPIRLTPTGVN-PPQPKLDSTLKTSPVTFPSDLSNLQV---SNR 67
 DB 2125 KIDLAEISIPRIMSDVDALRSKQWKTVDEYTK-RPDGSPFLDKQKLLPQNEANI 2183
 QY 68 PGRVYNQLINALVLYVGTQAIHIIH-NKGSTPEMSTITSAHMDI-----FQNLAV 118
 DB 2184 AGTRINAPLVNSLVYGMQVQQLQNKRNASASAOQMOQSLDVQIETATELFRNLVM 2243
 QY 119 DLDTEGRYLPLNAINQRLRYPNSTHTYFSCMTLYLPAEANTKAIQEOITRVLLRLIYNR 178
 DB 2244 NSDTEGRYLLNAINQRLRYPNSTHTYFSPFLILFSEANQEIQEOITRVLLRLIYNR 2303
 QY 179 PHPWGLITITIELIKNPAFKFNHGFVCAPEIKLFGSYAQCQMGQ 225
 DB 2304 PHPWGLITITIELIKNPRYSFWARSFTRCAPRIEIKLFEVSARSCGK 2350

Search completed: July 14, 2005, 20:32:01
 Job time : 83.5891 secs

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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:54:41 ; Search time 105.417 Seconds

(without alignments)
1196.043 Million cell updates/sec

Title: US-10-019-151C-3

Perfect score: 1738
Sequence: 1 MARKELSKARGQRTLLSAT.....RGASQELKAVRSVSEBQC 326

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1738	100.0	326	4 AAB20091	Aab20091 Human hyd
2	1733	99.7	326	4 AAM93915	Aam93915 Human pol
3	1733	99.7	326	8 ADL32038	ADL32038 Human pro
4	1725	99.3	339	2 AAY29331	Aay29331 Human sec
5	1725	99.3	339	4 AUA39057	Aua39057 Human sec
6	1725	99.3	339	5 ABB55766	Abb55766 Human pol
7	1450.5	83.5	275	4 AAM93907	Aam93907 Human pol
8	1450.5	83.5	275	8 ADL32022	ADL32022 Human pro
9	1232	70.9	323	6 ABU19723	ABU19723 Human sec
10	1232	70.9	323	6 ABP99774	ABP99774 Human sec
11	1232	70.9	323	6 ABR01267	ABR01267 Human gen
12	1232	70.9	323	6 ADA98352	ADA98352 Human sec
13	1232	70.9	324	3 AAB51635	Aab51635 Human sec
14	1086	62.5	330	5 ABB88807	Abb88807 Human pol
15	987.5	56.8	343	4 AAM93674	Aam93674 Human pol
16	987.5	56.8	343	8 ADL31529	ADL31529 Human pro
17	887.5	51.1	304	6 ADA14417	Ada14417 Mouse spe
18	669.5	38.5	357	5 ABB97772	Abb97772 Human sec
19	669.5	38.5	359	6 ABB75926	Abb75926 Human sec
20	669.5	38.5	359	6 ABB75771	Abb75771 Human sec
21	657.5	37.8	285	3 AAY66710	Aay66710 Membrane
22	657.5	37.8	285	4 AAU12395	Aau12395 Human PRO
23	657.5	37.8	285	4 AAB94851	Aab94851 Human PRO
24	657.5	37.8	285	4 AAB65233	Aab65233 Human PRO
25	657.5	37.8	285	6 ABUS8048	Abus8048 Human PRO

26	657.5	37.8	285	6 ABUS9126	Abus9126 Novel hum
27	657.5	37.8	285	6 ABUS2638	Abus2638 Human sec
28	657.5	37.8	285	6 ABO17839	Abol17839 Novel hum
29	657.5	37.8	285	6 ABUS6057	Abus6057 Human sec
30	657.5	37.8	285	6 ABUS1393	Abus1393 Human PRO
31	657.5	37.8	285	6 ABUS1093	Abus1093 Human PRO
32	657.5	37.8	285	6 ABUS2524	Abus2524 Novel hum
33	657.5	37.8	285	6 ABUS6793	Abus6793 Human PRO
34	657.5	37.8	285	6 ABUS9874	Abus9874 Novel sec
35	657.5	37.8	285	6 ABUS9273	Abus9273 Human sec
36	657.5	37.8	285	6 ABO25970	Abos25970 Human PRO
37	657.5	37.8	285	6 ABO25064	Abos25064 Human sec
38	657.5	37.8	285	6 ABUS8979	Abus8979 Human sec
39	657.5	37.8	285	6 ABUS9357	Abus9357 Novel hum
40	657.5	37.8	285	6 ABUS9422	Abus9422 Novel hum
41	657.5	37.8	285	6 ABUS7069	Abus7069 Human sec
42	657.5	37.8	285	6 ABUS2188	Abus2188 Novel hum
43	657.5	37.8	285	6 ABUS10894	Abus10894 Human PRO
44	657.5	37.8	285	6 ABUS1646	Abus1646 Novel hum
45	657.5	37.8	285	6 ABUS8585	Abus8585 Human sec

ALIGNMENTS

RESULT 1
AAB20091
ID AAB20091 standard; protein; 326 AA.

AC AAB20091;

DT 23-APR-2001 (first entry)

DE Human hydrophobic domain-containing protein HP03371.

XX Human; hydrophobic domain; antiinflammatory; immunosuppressive;

XX Immunostimulant; vulnery; antitumor; antitumor; antitumor; antitumor;

KW hepatotropic; thrombolytic; antitumor; antitumor; antitumor; antitumor;

XX antitumor; gene therapy; diagnosis; membrane protein.

OS Homo sapiens.

PN WC000100824-A2.

PF 16-JUN-2000; 2000MO-JP003944.

PR 24-JUN-1999; 99JP-00178065.

PA (SAGA) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

PI Kato S, Kimura T;

DR WPI, 2001-123008/13.

XX N-PSDB; AAB20091.

PT New proteins with hydrophobic domains, useful for treating autoimmune

PS diseases, inflammatory diseases, wounds, burns, incisions and ulcers.

XX Claim 1; Page 89-90; 126pp; English.

CC The present sequence is that of a novel human protein having 2 putative

CC transmembrane domains. It is predicted from cDNA clone HP03371 (see

CC AAF30022), isolated from a lymphoma cell line U937 cDNA library. The

CC predicted 39 kDa protein shows 71.5% homology to mouse protein GSG1. The

CC invention provides human proteins (see AAB20089-96) having hydrophobic

CC domains indicative of secretory signals or membrane domains, and nucleic

CC acids (see AAF30020-27) encoding them. These are expected to have cell

CC proliferation, cell differentiation, immunostimulant or immunosuppressor,

CC haemopoietic regulating, tissue growth, activin, inhibin, chemotactic,

CC chemokinetic, haemostatic, thrombolytic, receptor/ligand.

CC antiinflammatory or antitumour activities (no evidence provided).
 CC Expression vectors, eukaryotic host cells and antibodies are also
 CC provided. The secreted or membrane proteins of the invention can be used
 CC as pharmaceuticals or antigens for preparing antibodies. Cells expressing
 CC them are utilized for detection of corresponding receptors or ligands,
 CC and in candidate drug screening

XX
 SQ Sequence 326 AA;

Query Match 100.0%; Score 1738; DB 4; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.7e-175;
 Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKMEISKAFSGQRTLLSAILSMLSLSPSTLSLNNYFVGQKVPKPLCEKGLAAKCPD 60
 DB 1 MAKMEISKAFSGQRTLLSAILSMLSLSPSTLSLNNYFVGQKVPKPLCEKGLAAKCPD 60
 QY 61 MPVSLDGDNTSTQEVVQYNNMETGDDRFSPFRSGMWLSCEETVEEPGERCRSFTELTP 120
 DB 61 MPVSLDGDNTSTQEVVQYNNMETGDDRFSPFRSGMWLSCEETVEEPGERCRSFTELTP 120
 QY 121 PAKREILMLSLGTQITTYIGLQFISFLLLTDLTLTGNPACGLKLSAFAVSSVLSGLLGM 180
 DB 121 PAKREILMLSLGTQITTYIGLQFISFLLLTDLTLTGNPACGLKLSAFAVSSVLSGLLGM 180
 QY 181 VAHMYTSQVFOATVNLGPEDMRPHVNNYGMAFYMAWLSFTCCMASAVTTTNTYTRMULF 240
 DB 181 VAHMYTSQVFOATVNLGPEDMRPHVNNYGMAFYMAWLSFTCCMASAVTTTNTYTRMULF 240
 QY 241 KCKHSKSPKENPNCPLPHHQCPRRLSSAAPVPGLTSTYHQYNQPIHSVSEGVDFYSEL 300
 DB 241 KCKHSKSPKENPNCPLPHHQCPRRLSSAAPVPGLTSTYHQYNQPIHSVSEGVDFYSEL 300
 QY 301 RNKGFORGASQELKEAVRSSVEEEOC 326
 DB 301 RNKGFORGASQELKEAVRSSVEEEOC 326

RESULT 2
 AAM93915
 ID AAM93915 standard; protein; 326 AA.

XX AAM93915;
 AC AAM93915;
 DT 06-NOV-2001 (first entry)
 XX Human polypeptide, SEQ ID NO: 4071.
 KW Human; full length cDNA; cDNA synthesis; oligo-capping.
 XX Homo sapiens.
 OS Homo sapiens.
 PN EP130094-A2.
 PD 05-SEP-2001.
 XX 07-JUL-2000; 2000EP-00114089.
 PF 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183765.
 XX (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 DR MPI; 2001-524255/58.
 DR N-PSDB; AAK94877.
 XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 XX

PS Claim 8; SEQ ID NO 4071; 1380bp + Sequence Listing; English.

XX The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO

XX
 SQ Sequence 326 AA;

Query Match 99.7%; Score 1733; DB 4; Length 326;
 Best Local Similarity 99.7%; Pred. No. 5.9e-175;
 Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAKMEISKAFSGQRTLLSAILSMLSLSPSTLSLNNYFVGQKVPKPLCEKGLAAKCPD 60
 DB 1 MAKMEISKAFSGQRTLLSAILSMLSLSPSTLSLNNYFVGQKVPKPLCEKGLAAKCPD 60
 QY 61 MPVSLDGDNTSTQEVVQYNNMETGDDRFSPFRSGMWLSCEETVEEPGERCRSFTELTP 120
 DB 61 MPVSLDGDNTSTQEVVQYNNMETGDDRFSPFRSGMWLSCEETVEEPGERCRSFTELTP 120
 QY 121 PAKREILMLSLGTQITTYIGLQFISFLLLTDLTLTGNPACGLKLSAFAVSSVLSGLLGM 180
 DB 121 PAKREILMLSLGTQITTYIGLQFISFLLLTDLTLTGNPACGLKLSAFAVSSVLSGLLGM 180
 QY 181 VAHMYTSQVFOATVNLGPEDMRPHVNNYGMAFYMAWLSFTCCMASAVTTTNTYTRMULF 240
 DB 181 VAHMYTSQVFOATVNLGPEDMRPHVNNYGMAFYMAWLSFTCCMASAVTTTNTYTRMULF 240
 QY 241 KCKHSKSPKENPNCPLPHHQCPRRLSSAAPVPGLTSTYHQYNQPIHSVSEGVDFYSEL 300
 DB 241 KCKHSKSPKENPNCPLPHHQCPRRLSSAAPVPGLTSTYHQYNQPIHSVSEGVDFYSEL 300
 QY 301 RNKGFORGASQELKEAVRSSVEEEOC 326
 DB 301 RNKGFORGASQELKEAVRSSVEEEOC 326

RESULT 3
 ADL32038
 ID ADL32038 standard; protein; 326 AA.

XX ADL32038;
 AC ADL32038;
 DT 20-MAY-2004 (first entry)
 XX Human protein encoded by a full length cDNA clone seqID 4071.
 DE Human protein encoded by a full length cDNA clone seqID 4071.
 KW human; medicine; signal transduction; glycoprotein; transcription;
 XX oligo-capping method.
 OS Homo sapiens.
 OS Homo sapiens.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 XX 07-JUL-2000; 2003EP-00025638.

PF 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183865.
 PR 07-JUL-2000; 2000EP-00114089.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX

XX Ora T, Nishikawa T, Isogai T, Hayashi K, Ichii S, Kawai Y,
PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H,
XX WPI; 2004-204755/20.
DR N-PSDB; ADL32037.
XX
PT New oligonucleotide primers (830 CDNA) useful for synthesizing full
length human CDNA.
PS Example 1; SEQ ID NO 4071; 1340bp; English.
XX
CC This invention relates to a novel primers useful for synthesizing full
length cDNA molecules that encode human proteins. Specifically, it refers
to secretory or membrane proteins that are potential therapeutic agents/
target molecules in the field of medicine, and in particular genes
encoding proteins that are associated with signal transduction,
CC glycoproteins and transcription. The present invention describes a method
for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polypeptide sequence is a full
length human protein of the invention.
XX
SQ Sequence 326 AA;
Query Match 99.7%; Score 1733; DB 8; Length 326;
Best Local Similarity 99.7%; Pred. No. 5.9e-175;
Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAKMEISKAESGQRTLLSAILSMLSLSTSTLSNMFVGTQKPKPLCEKGLAAKCPD 60
DB 1 MAKMEISKAESGQRTLLSAILSMLSLSTSTLSNMFVGTQKPKPLCEKGLAAKCPD 60
QY 61 MPVSLDDTNTSTQEVQYNNMETGDDRFPSRSGMWLSCEETVEBGERCRSFIELTP 120
DB 61 MPVSLDDTNTSTQEVQYNNMETGDDRFPSRSGMWLSCEETVEBGERCRSFIELTP 120
QY 121 PAKREILMLSLGTQITTYIGLOFISFLLLTDLLLTGNPACGLKLSAFAAVSSVLSGLGM 180
DB 121 PAKREILMLSLGTQITTYIGLOFISFLLLTDLLLTGNPACGLKLSAFAAVSSVLSGLGM 180
QY 181 VAHMYTSQVFOATVNLGPEBDMRPHVMYNGAFYMAMLFTCCMAAATTTNTTMYLLEF 240
DB 181 VAHMYTSQVFOATVNLGPEBDMRPHVMYNGAFYMAMLFTCCMAAATTTNTTMYLLEF 240
QY 241 KCHHSKSPKPNPCLPHHQCFFPRRLSSAAPTVGELTSTYHQYNQPHSVSEGVDFYSEL 300
DB 241 KCHHSKSPKPNPCLPHHQCFFPRRLSSAAPTVGELTSTYHQYNQPHSVSEGVDFYSEL 300
QY 301 RNKGFGASQELKEAVRSSVVEBEC 326
DB 301 RNKGFGASQELKEAVRSSVVEBEC 326

RESULT 4
AA29331
ID AA29331 standard; protein; 339 AA.
XX
AC AA29331;
XX
DT 29-SEP-1999 (first entry)
XX
DE Human secreted protein clone mt24_2 protein sequence.
XX
KW Human; secreted protein; nutrition; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; suppression; gene therapy;
KW haematopoiesis regulation; tissue growth; activin; inhibin; cadherin;
KW chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory;
KW tumour invasion suppressor; tumour inhibition.
XX
OS Homo sapiens.
XX
PN MO9937674-A1.
XX

PD 29-JUL-1999.
XX
XX 21-JAN-1999; 99MO-US001404.
XX
XX 22-JAN-1998; 98US-0072134P.
PR 20-JAN-1999; 99US-00235609.
XX
XX (GENY) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Merberg D,
PI Treacy M, Agostino MJ, Steininger RJ, Wong GG, Clark HP, Reichel K,
XX WPI; 1999-458682/38.
DR N-PSDB; AAX90446.
XX
PT New polynucleotides encoding secreted human proteins derived from, e.g.
fetal brain potentially used as immunostimulators.
XX
PS Claim 28; Page 122-123; 139pp; English.
XX
CC The present sequence represents a human secreted protein. Human secreted
protein polynucleotides and proteins are predicted to have biological
activities which would make them suitable for treating, preventing or
ameliorating medical conditions in humans and animals, although no
supporting data is given. Suggested activities include nutritional
activity, cytokine and cell proliferation/differentiation activity,
CC immune stimulating (e.g. as vaccine) or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
activity, cadherin/tumour invasion suppressor activity, and tumour
inhibition activity. The polynucleotides are also suited to be useful for
gene therapy
XX
SQ Sequence 339 AA;
Query Match 99.3%; Score 1725; DB 2; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.4e-174;
Matches 323; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 KMEISKAESGQRTLLSAILSMLSLSTSTLSNMFVGTQKPKPLCEKGLAAKCPD 62
DB 16 KMEISKAESGQRTLLSAILSMLSLSTSTLSNMFVGTQKPKPLCEKGLAAKCPD 75
QY 63 VSLDGDNTSTQEVQYNNMETGDDRFPSRSGMWLSCEETVEBGERCRSFIELTP 122
DB 76 VSLDGDNTSTQEVQYNNMETGDDRFPSRSGMWLSCEETVEBGERCRSFIELTP 135
QY 123 KREILMLSLGTQITTYIGLOFISFLLLTDLLLTGNPACGLKLSAFAAVSSVLSGLGM 182
DB 136 KREILMLSLGTQITTYIGLOFISFLLLTDLLLTGNPACGLKLSAFAAVSSVLSGLGM 195
QY 183 HMYTSQVFOATVNLGPEBDMRPHVMYNGAFYMAMLFTCCMAAATTTNTTMYLLEF 242
DB 196 HMYTSQVFOATVNLGPEBDMRPHVMYNGAFYMAMLFTCCMAAATTTNTTMYLLEF 255
QY 243 KHSKSPKPNPCLPHHQCFFPRRLSSAAPTVGELTSTYHQYNQPHSVSEGVDFYSEL 302
DB 256 KHSKSPKPNPCLPHHQCFFPRRLSSAAPTVGELTSTYHQYNQPHSVSEGVDFYSEL 315
QY 303 KGFQASQELKEAVRSSVVEBEC 326
DB 316 KGFQASQELKEAVRSSVVEBEC 339

RESULT 5
AAU39057
ID AAU39057 standard; protein; 339 AA.
XX
AC AAU39057;
XX
DT 16-JAN-2002 (first entry)
XX

Human secreted protein mt24_2.

KM Human; secreted protein; antiinflammatory; immunosuppressive; nontropic;
 KM neuroprotective; antiarthritic; antimicrobial; vulnerary; cyostatic;
 KM antidiabetic; viricide; antifertility; anticoagulant; vasotropic;
 KM antiparkinsonian; immunostimulant; dermatological; antineumatic;
 KM antitumor; anticler; osteoprotic; tranquilizer; cerebroprotective;
 KM cytokine; cell proliferation; cell differentiation; immune deficiency;
 KM severe combined immunodeficiency; SCID tumour; autoimmune disorder;
 KM multiple sclerosis; rheumatoid arthritis; graft-versus-host disease;
 KM myeloid deficiency; wound healing; ulcer; peridontal disease;
 KM osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease;
 KM Huntington's disease; infection; cardiac disease; stroke; sepsis;
 KM inflammatory bowel disease; contraceptive; immunogen; food supplement;
 KM vaccine.

Homo sapiens.

PN WO200175068-A2.

11-OCT-2001. PD

22-MAR-2001; 2001WO-US009369.

30-MAR-2000; 2000US-00539330.

PR 04-DEC-2000; 2000US-00729674.

PA (GEMY) GENETICS INST INC.

PI Jacobs K, McCoy JM, Lavalie B, Collins-Racie LA, Evans C;

PI Fechtel K, Merberg

DR WPI; 2001-639363/

XX

PT such as autoimmune disorders (e.g.,

XX spectrum (see also Fig. 5B and C).
 XX Disclosure; Page 548-549; 619pp; English.
 XX The invention relates to novel human secreted proteins, the nucleic acids
 CC encoding them. The protein may exhibit cytokine, cell proliferation or
 CC cell differentiation activity or may induce production of other cytokines
 CC in certain cell populations and may exhibit immune stimulating or immune
 CC suppressing activity, which is useful for the treatment of various immune
 CC deficiencies and disorders e.g. severe combined immunodeficiency (SCID),
 CC autoimmune disorders e.g. multiple sclerosis, systemic lupus
 CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation.
 CC The proteins are also useful in the treatment of diseases and disorders
 CC including tissue, skin and organ transplantation and in graft-versus-host
 CC diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid
 CC cell deficiencies, wound healing and tissue repair, in the treatment of
 CC burns, incisions and ulcers; as well as in treatment of periodontal
 CC disease, osteoporosis or osteoarthritis, mediated by inflammatory
 CC processes, diseases of the peripheral nervous system, Alzheimer's,
 CC Parkinson's disease, Huntington's disease, amyotrophic lateral
 CC sclerosis, and Shy-Drager syndrome, infections, infection of cardiac and
 CC central nervous system vessel e.g. stroke, sepsis, inflammatory bowel
 CC disease, ulcers, bone regeneration. The protein, having activin- or
 CC inhibin-related activities is useful as a contraceptive based on the
 CC ability of inhibins to decrease fertility in female mammals and decrease
 CC spermatogenesis in male mammals. The proteins and nucleic acids are also
 CC useful as food supplements. The present sequence represents a secreted
 CC protein of the invention

Sequence 339 AA;

Query Match	99.3%	Score 1725;	DB 4;	Length 339;
Best Local Similarity	99.7%	Pred. No. 4.4e-174;		
Matches 323; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	KHMLKRAFSQORPLLSAILSMLSLSPSTTSLSNWFWGQKVKPKCEKGLAKGDM	62
Db	16	EMELSKAFSGQRLLSAILSMLSLSPSTTSLSNWFWGQKVKPKCEKGLAKGDM	75
QY	63	VSLDGDTNSTOEVQYNNWETGDDRFPSRSPRSGMMLSCBETVEPGBCRSPLELTPPA	122
Db	76	VSLDGDTNSTOEVQYNNWETGDDRFPSRSPRSGMMLSCBETVEPGBCRSPLELTPPA	135
QY	123	KREILMLSLGTOTTYTGLOFISFLLLDLTLTGPAQGLKLSAPAAVSSVLSGLGMA	182
Db	136	KREILMLSLGTOTTYTGLOFISFLLLDLTLTGPAQGLKLSAPAAVSSVLSGLGMA	195
QY	183	HMAYSQVFOATVNLGPEDMRPHVMNYGMAFYAMLSPTCCMAASVTTFNTRYRMLEFKC	242
Db	196	HMAYSQVFOATVNLGPEDMRPHVMNYGMAFYAMLSPTCCMAASVTTFNTRYRMLEFKC	255
QY	243	KHASKSPENDNCLPHHQCFPRRLSSAPATVQPLTSLSYQYNOPRHSVSEGVDSYELRN	302
Db	256	KHASKSPENDNCLPHHQCFPRRLSSAPATVQPLTSLSYQYNOPRHSVSEGVDSYELRN	315
QY	303	KGFORGASDELKAVSSVVEEQC	326
Db	316	KGFORGASDELKAVSSVVEEQC	339

RESULT 6
ABB55766

AC ABB55766;

DT 14-FEB-2002 (first entry)

DE Human polypeptide SEQ ID NO 138.

Human; clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulvare; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; Crohn's disease; cytotoxic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory.

Homo sapiens.

PN US2001039335-A1.

PD 08-NOV-2001

PF 04-DEC-2000; 2000US-00729674.

PR	26-NOV-1997,	97US-0126425P
AA	04-DEC-1997,	97US-0067454P
PR	20-DEC-1997,	97US-0068379P
PR	02-JAN-1998,	98US-0070346P
PR	07-JAN-1998,	98US-0070643P
PR	08-JAN-1998,	98US-0070755P
PR	13-JAN-1998,	98US-0071304P
PR	22-JAN-1998,	98US-0072134P
PR	18-FEB-1998,	98US-0073035P
PR	18-FEB-1998,	98US-0075038P
PR	23-MAR-2000,	98US-0019786B
PR		2000US-00539330

XX	(JACO/)	JACOBS K.
PA	(MCCO/)	MCCOY J M.
PA	(LAVA/)	LAVALLE E R.
PA	(COLL/)	COLLINS-RACIE L A
PA	(EVAN/)	EVANS C.
PA	(MERB/)	MERBERG D.
PA	(TREB/)	TREARY M.

PA (AGOSTINO M J.
PA (STEL/) STEININGER R J.
PA (SPAU/) SPAULDING V.
PA (WONG/) WONG G G.
PA (CLAR/) CLARK H.
PA (FECH/) FECHTEL K.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C,
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V,
PI Wong GG, Clark H, Fechtel K,
XX
DR WPI; 2002-040725/05.
DR N-PSDB; ABA90944.
XX
XX
PT New secreted proteins and encoding polynucleotides, useful in gene
PT therapies, particularly for preventing or treating autoimmune disorders,
PT cancer, graft-versus-host disease, wound, osteoporosis, stroke or
PT inflammation.
XX
XX
PS Disclosure; Page 276-277; 349pp; English.
XX
XX The invention relates to isolated polynucleotides (ABA90876-ABA90968 and
XX ABA90980) and encoded proteins (ABBS5698-ABBS5800), especially
XX polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and
XX proteins SEQ ID NO 2 (ABBS5698) and SEQ ID NO 20 (ABBS5707) contained in
XX clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1
XX are deposited with the American Type Culture Collection (ATCC) with
XX accession number 98599. The polynucleotides and encoded polypeptides have
XX cytostatic, anti-inflammatory, immunomodulator, vlnetary,
XX neuroprotective, activin, inhibin, chemotactic, rheumatoid, thrombolytic
XX and anti-inflammatory activity and acting as cytokine modulators,
XX hemostasis regulators, tissue growth modulators and/or cadherin
XX suppressors. The polypeptides and polynucleotides are useful in gene
XX therapies, particularly for preventing, treating or ameliorating any of
XX the following diseases: immune deficiency and disorders; e.g. bacterial
XX or fungal infections, autoimmune disorders, cancer, systemic lupus
XX erythematosus or graft-versus-host disease; myeloid or lymphoid cell
XX deficiencies; wound, burns, incisions and ulcers, osteoporosis or
XX osteoarthritis; central and peripheral nervous system diseases and
XX neuropathies; e.g. Alzheimer's, Parkinson's disease, Huntington's
XX disease, amyotrophic lateral sclerosis or Shy-Drager syndrome;
XX haemophilia, cardiac infarction or stroke; inflammations, shock, sepsis
XX or systemic inflammatory response syndrome, ischemia-reperfusion injury,
XX endotoxin lethality, arthritis, inflammatory bowel disease or Crohn's
XX disease; or tumours or cancers, pemphigus vulgaris or pemphigus foliaceus
XX
XX Sequence 339 AA;
XX
Query Match 99.3%; Score 1725; DB 5; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.4e-174;
Matches 323; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 KHELKRAFGSGRTLLSLNLSLSFSTSLNSYFVGQKPKPLCEKGLAKCPDM 62
DB 16 EMLSKAFSGQRTLLSLNLSLSFSTSLNSYFVGQKPKPLCEKGLAKCPDM 75
QY 63 VSLDGTNTSTQEVQVQNMETGDRFGRSFRSGMWSCEETVEEPEGRCRSPFIELTP 122
DB 76 VSLDGTNTSTQEVQVQNMETGDRFGRSFRSGMWSCEETVEEPEGRCRSPFIELTP 135
QY 123 KREILMLSLGTQITTYIGLQFISFLILLTDLITGNPACGLKSAFAVSSVLSGLGMVA 182
DB 136 KREILMLSLGTQITTYIGLQFISFLILLTDLITGNPACGLKSAFAVSSVLSGLGMVA 195
QY 183 HMMYSGVFOATVNLGPEDMRPHVWNYGMAFYMAWLSFTCCMAASAVTTFTNTYTRVLEFK 242
DB 196 HMMYSGVFOATVNLGPEDMRPHVWNYGMAFYMAWLSFTCCMAASAVTTFTNTYTRVLEFK 255
QY 243 KHKSPKREANPCPHHQCPRRRLSSAAPTGGPLTSHQYHNPYHSVSGVDPFYSELRN 302
DB 256 KHKSPKREANPCPHHQCPRRRLSSAAPTGGPLTSHQYHNPYHSVSGVDPFYSELRN 315
QY 303 KGFORGASQELKKAIVSSVEEBC 326

DB 316 KGFORGASQELKKAIVSSVEEBC 339
|||||
RESULT 7
ID AAM93907 standard; protein; 275 AA.
XX AAM93907
AC AAM93907;
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 4055.
XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping.
XX Homo sapiens.
XX
XX EP1130094-A2.
XX
XX 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-00114089.
XX
XX 08-JUL-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-00118774.
XX 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
PI Oca T, Nishikawa T, Isogai T, Hayaishi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H,
DR WPI; 2001-524255/58.
XX N-PSDB; AAK94869.
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
XX Claim 8; SEQ ID NO 4055; 1380pp + Sequence listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX been determined. Primers for synthesizing the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is a polypeptide encoded by a full length
XX human cDNA of the invention. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in CD-ROM
XX format directly from EPO
XX
XX Sequence 275 AA;
XX
Query Match 83.5%; Score 1450.5; DB 4; Length 275;
Best Local Similarity 84.0%; Pred. No. 4.7e-145;
Matches 274; Conservative 1; Mismatches 0; Indels 51; Gaps 1;
QY 1 MAAMELSKAFSGQRTLLSLNLSLSFSTSLNSYFVGQKPKPLCEKGLAKCPD 60
DB 1 MAAMELSKAFSGQRTLLSLNLSLSFSTSLNSYFVGQKPKPLCEKGLAKCPD 60
QY 61 MPVSLDGTNTSTQEVQVQNMETGDRFGRSFRSGMWSCEETVEEPEGRCRSPFIELTP 120
DB 61 MPVSLDGTNTSTQEVQVQNMETGDRFGRSFRSGMWSCEETVEEPEGRCRSPFIELTP 120
QY 121 PAKREILMLSLGTQITTYIGLQFISFLILLTDLITGNPACGLKSAFAVSSVLSGLGM 180
DB 121 PAKR-----GLLGM 129
QY 181 VAMMYSGVFOATVNLGPEDMRPHVWNYGMAFYMAWLSFTCCMAASAVTTFTNTYTRVLEP 240

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Db      130 VAHMMYSQVFOATVNLGPEDMRPHVWNYGMAFYMAWLSFTCCMASAVTTFTNTTTRVLVEF 189
Qy      241 KCKHKSFPKFNENCLPHHQCPRRLSSAAPTGVLTSTYHOYHNPPIHSVSEGVDFYSEL 300
Db      190 KCKHKSFPKFNENCLPHHQCPRRLSSAAPTGVLTSTYHOYHNPPIHSVSEGVDFYSEL 249
Qy      301 RNKGFORGASQELKEAVRSSVEEQC 326
Db      250 RNKGFORGASQELKEAVRSSVEEQC 275

RESULT 8
ADL32022
ID      ADL32022 standard; protein; 275 AA.
AC      ADL32022;
DT      20-MAY-2004 (first entry)
XX      Human protein encoded by a full length cDNA clone SeqID 4055.
XX      human; medicine; signal transduction; glycoprotein; transcription;
XX      oligo-capping method.
XX      Homo sapiens.
XX      EPI396543-A2.
XX      10-MAR-2004.
XX      07-JUL-2000; 2003EP-00025638.
XX      08-JUL-1999; 99JP-00194486.
XX      11-JAN-2000; 2000JP-00118774.
XX      02-MAY-2000; 2000JP-00183865.
XX      07-JUL-2000; 2000EP-00114089.
XX      (REAS-) RES ASSOC BIOTECHNOLOGY.
XX      Ota T, Nishikawa T, Iacgai T, Hayashi K, Ishii S, Kawai Y,
XX      Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX      MPI; 2004-204755/20.
XX      N-PSDB; ADL32021.
XX      New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX      length human cDNAs.
XX      Example 1; SEQ ID NO 4055; 1340pp; English.
XX      This invention relates to a novel primers useful for synthesizing full
XX      length cDNA molecules that encode human proteins. Specifically, it refers
XX      to secretory or membrane proteins that are potential therapeutic agents/
XX      target molecules in the field of medicine, and in particular genes
XX      encoding proteins that are associated with signal transduction,
XX      glycoproteins and transcription. The present invention describes a method
XX      for efficiently cloning a full length human cDNA from both the 5' and 3'
XX      ends using the oligo-capping method. This polypeptide sequence is a full
XX      length human protein of the invention.
XX      Sequence 275 AA;
SQ      Query Match      83.5%; Score 1450.5; DB 8; Length 275;
        Best Local Similarity 84.0%; Pred. No. 4,7e-145;
        Matches 274; Conservative 1; Mismatches 0; Indels 51; Gaps 1;

Qy      1 MAHMBLSKAFSGGRTLSLISLMSLSFSTLSLNNYFWGQKVPKPLCEKGLAKCFD 60
Db      1 MAHMBLSKAFSGGRTLSLISLMSLSFSTLSLNNYFWGQKVPKPLCEKGLAKCFD 60
Qy      61 MPVSLDGDNTNSTQEVVQYVWMTGDDRFSPFRSGMWLSCEBTEVEPGERCRSFTELTTP 120

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Db      61 MPVSLDGDNTNSTQEVVQYVWMTGDDRFSPFRSGMWLSCEBTEVEPGERCRSFTELTTP 120
Qy      121 PAKREILMISLSTQTYTIGLOPISFLLLTDLTLGNPACGKLSAPAAVSSVLSGLGM 180
Db      121 PAKR-----GLIGM 129
Qy      181 VAHMMYSQVFOATVNLGPEDMRPHVWNYGMAFYMAWLSFTCCMASAVTTFTNTTTRVLVEF 240
Db      130 VAHMMYSQVFOATVNLGPEDMRPHVWNYGMAFYMAWLSFTCCMASAVTTFTNTTTRVLVEF 189
Qy      241 KCKHKSFPKFNENCLPHHQCPRRLSSAAPTGVLTSTYHOYHNPPIHSVSEGVDFYSEL 300
Db      190 KCKHKSFPKFNENCLPHHQCPRRLSSAAPTGVLTSTYHOYHNPPIHSVSEGVDFYSEL 249
Qy      301 RNKGFORGASQELKEAVRSSVEEQC 326
Db      250 RNKGFORGASQELKEAVRSSVEEQC 275

RESULT 9
ABJ19723
ID      ABJ19723 standard; protein; 323 AA.
AC      ABJ19723;
DT      03-APR-2003 (first entry)
XX      Human secreted protein amino acid sequence - SEQ ID NO 191.
XX      Human; protein therapy; immediate hypersensitivity diseases;
XX      allergic disorder; asthmatic disorder; gene therapy; secreted protein;
XX      hay fever; allergic conjunctivitis; allergic rhinitis;
XX      binding partner identification; chromosome identification;
XX      radiation hybrid mapping; long-range restriction mapping.
XX      Homo sapiens.
XX      WO200271188-A2.
XX      03-OCT-2002.
XX      26-MAR-2002; 2002WO-US009239.
XX      27-MAR-2001; 2001US-0278650P.
XX      12-SEP-2001; 2001US-00950082.
XX      12-SEP-2001; 2001US-00950083.
XX      (HDMA-) HUMAN GENOME SCI INC.
XX      Rosen CA, Ruben SM;
XX      MPI; 2003-175010/17.
XX      Use of human secreted proteins and nucleic acids for preparing a
XX      diagnostic or pharmaceutical composition for diagnosing or treating
XX      allergic or asthmatic disorders, e.g. asthma, hay fever, or allergic
XX      conjunctivitis or rhinitis.
XX      Claim 1; Page 644-645; 823pp; English.
XX      The invention comprises the amino acid and coding sequences of human
XX      secreted proteins. The DNA and protein sequences of the invention are
XX      useful for the diagnosis and treatment of allergic disorders, asthmatic
XX      disorders and immediate hypersensitivity diseases (e.g. hay fever,
XX      allergic conjunctivitis and allergic rhinitis). The proteins of the
XX      invention are also useful for identifying a binding partner. The nucleic
XX      acids of the invention are also useful for chromosome identification,
XX      radiation hybrid mapping or long-range restriction mapping. The present
XX      amino acid sequence represents a human secreted protein of the invention
XX      Sequence 323 AA;
SQ      Query Match      70.9%; Score 1232; DB 6; Length 323;

```

Best Local Similarity 73.0%; Pred. No. 9.8e-122;
Matches 251; Conservative 10; Mismatches 41; Indels 42; Gaps 6;

QY 4 MELSKAFSGQRTLLSAILSMLSLSPSTTSLSNVFWGTQKVPKPCCKGLAKCFDMPV 63
DB 1 MELSKAFSGQRTLLSAILSMLSLSPSTTSLSNVFWGTQKVPKPCCKGLAKCFDMPV 60
QY 64 SLDDNTSTQEVVQVNWETGDDRFSPFRSGMWLSCBETVEBGRCSFIETLTPAK 123
DB 61 SLDDNTSTQEVVQVNWETGDDRFSPFRSGMWLSCBETVEBGRCSFIETLTPAK 120
QY 124 RELWLSLGTQIYIGLQFISFLLLTDLLTGNPACGLKLSAPAVSVLSGLL----- 178
DB 121 RKNPMVTPG-NADHLRTSIHQLEPATNRLATHEPC-----LMAQTERLCCCFCLCVRS 174
QY 179 -GNVAHMYTQVQVQATVNLGPEDMRPHVWNYGAFYV-----AMLSFT-----CC 222
DB 175 PGDVAHMYTQVQVQATVNLGPEDMRPHVWNYGAFYVACSPKSAARLSPXSTXTPGWC 234
QY 223 MASAVTTFNTYTMVLEFPKCKSKSPKPNCLPHHOCPPRLSSAAPVGLTSYHOY 282
DB 235 WSSASIV-----KSPKPNCLPHHOCPPRLSSAAPVGLTSYHOY 279
QY 283 HNOPIHVSBGVDFYSELNKGFORGASQELKEAVSVSEBQC 326
DB 280 HNOPIHVSBGVDFYSELNKGFORGASQELKEAVSVSEBQC 323

RESULT 10

ABP9774
ID ABP9774 standard; protein; 323 AA.

XX AC ABP9774;

XX DT 26-MAR-2003 (first entry)

XX DE Human secreted protein SEQ ID NO 718.

XX XX Human; secreted protein; nocrotic; neuroprotective; cytosolic;
KW Vitruide; dermatological; immunosuppressive; anti-inflammatory; anti-HIV;
KW vulnary; antibacterial; antiparkinsonian; antichilling; antianemic;
KW antituberc; cancer; antineumatic; hepatocytic; cerebroprotective;
KW antiinflammatory; antiallergic; antidiabetic; antilucer; anticonvulsant;
KW antifungal; antiparasitic; cardiac; immune disorder; infection; vaccine;
KW cardiovascular disorder; neurological disease; nephrotoxic;
KW gene therapy.

XX OS Homo sapiens.

XX PN WO200277186-A2.

XX PD 03-OCT-2002.

XX PF 26-MAR-2002; 2002WO-US009188.

XX PR 27-MAR-2001; 2001US-0278650P.

XX PR 12-SEP-2001; 2001US-00950082.

XX PR 12-SEP-2001; 2001US-00950083.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI, 2003-040583/03.

XX DR N-PSDB; ABZ67195.

XX PT New human secreted proteins encoded by genes contained in cDNA clones
PT (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g. AIDS,
PT multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or
PT West Nile fever.

XX PS Claim 1; Page 1479; 2423pp; English.

CC The invention relates to novel human genes (ABZ66891-ABZ68209) and the
CC encoded secreted proteins (ABP9470-ABP99872) useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The genes are isolated from a range of human tissues disclosed
CC in the specification. The nucleic acids, protein, antibodies and
CC (ant)agonists are useful in the diagnosis, treatment and prevention of:
CC (a) cancer, e.g. breast and ovarian cancer and other cancers of the
CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC lung or urogenital; (b) immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g.
CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
CC bacterial, fungal and parasitic infections

XX SQ Sequence 323 AA;

Query Match 70.9%; Score 1232; DB 6; Length 323;

Best Local Similarity 73.0%; Pred. No. 9.8e-122;
Matches 251; Conservative 10; Mismatches 41; Indels 42; Gaps 6;

QY 4 MELSKAFSGQRTLLSAILSMLSLSPSTTSLSNVFWGTQKVPKPCCKGLAKCFDMPV 63
DB 1 MELSKAFSGQRTLLSAILSMLSLSPSTTSLSNVFWGTQKVPKPCCKGLAKCFDMPV 60
QY 64 SLDDNTSTQEVVQVNWETGDDRFSPFRSGMWLSCBETVEBGRCSFIETLTPAK 123
DB 61 SLDDNTSTQEVVQVNWETGDDRFSPFRSGMWLSCBETVEBGRCSFIETLTPAK 120
QY 124 RELWLSLGTQIYIGLQFISFLLLTDLLTGNPACGLKLSAPAVSVLSGLL----- 178
DB 121 RKNPMVTPG-NADHLRTSIHQLEPATNRLATHEPC-----LMAQTERLCCCFCLCVRS 174
QY 179 -GNVAHMYTQVQVQATVNLGPEDMRPHVWNYGAFYV-----AMLSFT-----CC 222
DB 175 PGDVAHMYTQVQVQATVNLGPEDMRPHVWNYGAFYVACSPKSAARLSPXSTXTPGWC 234
QY 223 MASAVTTFNTYTMVLEFPKCKSKSPKPNCLPHHOCPPRLSSAAPVGLTSYHOY 282
DB 235 WSSASIV-----KSPKPNCLPHHOCPPRLSSAAPVGLTSYHOY 279
QY 283 HNOPIHVSBGVDFYSELNKGFORGASQELKEAVSVSEBQC 326
DB 280 HNOPIHVSBGVDFYSELNKGFORGASQELKEAVSVSEBQC 323

RESULT 11

ABR01267
ID ABR01267 standard; protein; 323 AA.

XX AC ABR01267;

XX DT 12-MAY-2003 (first entry)

XX DE Human gene 321-encoded secreted protein HTEB69, SEQ ID NO: 748.

XX XX Human; secreted protein; cancer; tumour; hyperproliferative disorder;
KW autoimmune disorder; inflammation; angiotensin diseases; AIDS;
KW acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;
KW drug screening; chromosome identification; chromosome mapping;
KW cytotoxic; gene therapy; antiinflammatory; immunomodulator; anti-HIV;
KW antianemic; vulnary.

XX OS Homo sapiens.

XX PN WO200277013-A2.

XX PD 03-OCT-2002.

XX PF 26-MAR-2002; 2002WO-US009370.

XX PR 27-MAR-2001; 2001US-0278650P.

PR 12-SEP-2001; 2001US-00950082.
 PR 12-SEP-2001; 2001US-00950083.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 DR WPI: 2003-040578/03.
 DR N-PSDB; AB273601.
 PT New human secreted proteins and nucleic acid, useful for detecting or
 PT treating cancer or other hyperproliferative disorders, autoimmune
 PT disorders, inflammatory disorders, HIV disease, hepatitis or anemia.
 XX
 PS Claim 13; Page 1479; 2474bp; English.
 XX
 XX AB273281-AB273697 represent cDNAs corresponding to 391 human secreted
 CC protein genes, and ABP00947-ABP01363 represent the proteins they encode.
 CC AB273698-AB274687 represent human secreted protein genomic fragments. The
 CC invention also encompasses antibodies specific for the secreted proteins,
 CC the use of the secreted proteins in drug screening and recombinant
 CC vectors and host cells comprising a nucleic acid of the invention. The
 CC secreted proteins are thought to be involved in biological activities
 CC associated with cellular signalling, cellular differentiation, cell
 CC migration, prohormone activation and neurotransmitter activity. The
 CC secreted proteins, nucleic acid encoding them, antibodies or antibody
 CC fragments specific for the secreted proteins, and modulators of protein
 CC activity are useful for diagnosing or treating cancers or other
 CC hyperproliferative disorders. Additionally, the secreted proteins and
 CC their nucleic acids may also be used in the treatment of autoimmune
 CC disorders, inflammatory disorders, diseases involving angiogenesis, AIDS
 CC (acquired immunodeficiency syndrome), hepatitis, anemia, and to promote
 CC wound healing. Nucleic acids of the invention may be used for chromosome
 CC identification, chromosome mapping, in gene therapy, for identifying
 CC individuals from minute biological samples, as hybridisation probes, and
 CC as molecular weight markers. The present sequence represents a human
 CC secreted protein of the invention
 XX
 XX Sequence 323 AA:
 Query Match 70.9%; Score 1232; DB 6; Length 323;
 Best Local Similarity 73.0%; Pred. No. 9.8e-122;
 Matches 251; Conservative 10; Mismatches 41; Indels 42; Gaps 6;
 QY 4 MELSKAFSGQRTLLSAILSMLSLSFSTSLSNVYFVGQKPKLCEKGLAAKCFDMPV 63
 DB 1 MELSKAFSGQRTLLSAILSMLSLSFSTSLSNVYFVGQKPKLCEKGLAAKCFDMPV 60
 QY 64 SLDGDNTSTQEVVQYNNMETGDRFSPFRSGMWLSCEETVEEGERCRSFIELTPPAK 123
 DB 61 SLDGDNTSTQEVVQYNNMETGDRFSPFRSGMWLSCEETVEEGERCRSFIELTPPAK 120
 QY 124 REILWLSLGTQITTYIGLQFISFLLLTDLTLGNPACGLKSAFAVSSVLSGLT----- 178
 DB 121 RENPWYIIPG-NADHLHRTSIHQLPATNRLATMHEPC-----LMAQTERLCCCFPCPVRS 174
 QY 179 -GNVAHMYTSQVFOATVNLGPEDMRPHYWNYGMAFYM-----AWLSFT-----CC 222
 DB 175 PGDVAHMYTSQVFOATVNLGPEDMRPHYWNYGMAFYMACSPSYAAMRRLSPXSTYTPGWC 234
 QY 223 MASAATTTPTNYTMYLVEFKCKSKSPKPNENCLPHHOCPPRLSSAAPTGVGLTSTYHOY 282
 DB 235 WSSSAATV-----KSKPENKCLPHHOCPPRLSSAAPTGVGLTSTYHOY 279
 QY 283 HNPPIHSVSEGVDFYSELNKGFORGASQELKEAVSSVEEBC 326
 DB 280 HNPPIHSVSEGVDFYSELNKGFORGASQELKEAVSSVEEBC 323
 RESULT 12
 ADA98352
 ID ADA98352 standard; protein; 323 AA.
 XX

AC ADA98352;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein sequence #193.
 XX
 KW human; secreted protein; cardiovascular disorder; arrhythmia;
 KW atherosclerosis; stroke; endocarditis; congestive heart failure;
 KW rheumatic heart disease; cardiomyopathy; haemorrhoids; varicose veins;
 KW migraine; thrombosis; neural disorder; immune system disorder;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; renal disorder; proliferative disorder; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2003004623-A2.
 XX
 PD 16-JAN-2003.
 XX
 XX 26-MAR-2002; 2002WO-US009922.
 PF
 XX 27-MAR-2001; 2001US-0278650P.
 PR 12-SEP-2001; 2001US-00950082.
 PR 12-SEP-2001; 2001US-00950083.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 DR WPI: 2003-247946/24.
 XX
 PT New human secreted polypeptide and nucleic acid molecules, useful for
 PT diagnosing, preventing, prognosticating or treating cardiovascular
 PT disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or
 PT thrombosis).
 XX
 PS Claim 1; SEQ ID NO 460; 1572bp; English.
 XX
 CC The invention comprises the amino acid and coding sequence of human
 CC secreted proteins. The DNA and protein sequences of the invention are
 CC useful in the treatment of cardiovascular disorders, such as: arrhythmia,
 CC atherosclerosis, stroke, endocarditis, congestive heart failure,
 CC rheumatic heart disease, cardiomyopathy, haemorrhoids, varicose veins,
 CC migraine, or thrombosis. The DNA and protein sequences may also be used
 CC for treating or preventing: neural disorders, immune system disorders,
 CC muscular disorders, reproductive disorders, gastrointestinal disorders,
 CC pulmonary disorders, renal disorders, proliferative disorders and/or
 CC cancerous diseases. The present amino acid sequence represents a human
 CC secreted protein of the invention. NOTE: The present sequence is shown on
 CC the WIPO website.
 XX
 XX Sequence 323 AA:
 Query Match 70.9%; Score 1232; DB 6; Length 323;
 Best Local Similarity 73.0%; Pred. No. 9.8e-122;
 Matches 251; Conservative 10; Mismatches 41; Indels 42; Gaps 6;
 QY 4 MELSKAFSGQRTLLSAILSMLSLSFSTSLSNVYFVGQKPKLCEKGLAAKCFDMPV 63
 DB 1 MELSKAFSGQRTLLSAILSMLSLSFSTSLSNVYFVGQKPKLCEKGLAAKCFDMPV 60
 QY 64 SLDGDNTSTQEVVQYNNMETGDRFSPFRSGMWLSCEETVEEGERCRSFIELTPPAK 123
 DB 61 SLDGDNTSTQEVVQYNNMETGDRFSPFRSGMWLSCEETVEEGERCRSFIELTPPAK 120
 QY 124 REILWLSLGTQITTYIGLQFISFLLLTDLTLGNPACGLKSAFAVSSVLSGLT----- 178
 DB 121 RENPWYIIPG-NADHLHRTSIHQLPATNRLATMHEPC-----LMAQTERLCCCFPCPVRS 174
 QY 179 -GNVAHMYTSQVFOATVNLGPEDMRPHYWNYGMAFYM-----AWLSFT-----CC 222
 DB 175 PGDVAHMYTSQVFOATVNLGPEDMRPHYWNYGMAFYMACSPSYAAMRRLSPXSTYTPGWC 234

Oy	223	MASAIATFNTYTRMVLFPKCKSKSPKRNENCCIPHHQCCPRLLSSAAPVGLTSTYHOY	282
Db	225	WSSSAISIV-----KSPKRNENCCIPHHQCCPRLLSSAAPVGLTSTYHOY	279
Oy	283	HNQPIHSVEGYDPFYSBELRNKGFQRAQAGCELKEAVSSVVEEOC	326
Db	280	HNQPIHSVEGYDPFYSBELRNKGFQRAQAGCELKEAVSSVVEEOC	323
RESULT 13			
ID	AAB51635		
XX	AAB51635	standard; protein; 324 AA.	
AC	AAB51635;		
XX			
DT	26-FEB-2001	(first entry)	
XX			
DE	Human secreted protein sequence encoded by gene 16 SEQ ID NO:75.		
XX			
KM	Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;		
KM	antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;		
KM	cerebroprotective; neutrotic; neuroprotective; antibacterial; virucide;		
KM	fungicide; ophthalmological; gene therapy; autoimmune disease; infection;		
KM	hyperproliferative disorder; cardiovascular disorder; angiogenesis;		
KM	cerebrovascular disorder; nervous system disorder; ocular disorder;		
KM	wound healing; skin aging; food additive; preservative.		
XX			
OS	Homo sapiens.		
XX			
PN	MO200061620-A1.		
XX			
PD	19-OCT-2000.		
XX			
PP	06-APR-2000; 2000WO-US009069.		
XX			
PR	09-APR-1999; 99US-0128702P.		
PR	20-JAN-2000; 2000US-0177049P.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
PA	(ROSE/) ROSEN C A.		
XX			
PI	Rosen CA, Ruben SM, Komatsuulis G;		
XX			
DR	WPI: 2000-619225/59.		
DR	N-PSDB; AAC93379.		
PT	Isolated nucleic acid molecule encoding a human secreted protein is used		
PT	in preventing, treating or ameliorating a medical condition.		
XX			
XX	Claim 11; Page 472-473; 540pp; English.		
CC	The polynucleotide sequences given in AAC93364 to AAC93412 encode the		
CC	human secreted proteins given in AAB51620 to AAB51668. AAB51669 to		
CC	AAB51722 represent human secreted polypeptide sequences and proteins		
CC	homologous to them, which are given in the exemplification of the present		
CC	invention. Human secreted proteins have activities based on the tissues		
CC	and cells the genes are expressed in. Examples of activities include:		
CC	antiarthritic; immunosuppressive; antirheumatic; antiproliferative;		
CC	cytostatic; cardiant; vasotropic; cerebroprotective; neutrotic;		
CC	neuroprotective; antibacterial; virucide; fungicide; and		
CC	ophthalmological. The polynucleotides and polypeptides can be used to		
CC	prevent, treat or ameliorate a medical condition in e.g. humans, mice,		
CC	rabbit, goats, horses, cats, dogs, chickens or sheep. They are also used		
CC	in diagnosing a pathological condition or susceptibility to a		
CC	pathological condition. Disorders which are diagnosed or treated include		
CC	autoimmune diseases, hyperproliferative disorders, cardiovascular		
CC	disorders, cerebrovascular disorders, angiogenesis, nervous system		
CC	disorders, infections caused by bacteria, viruses and fungi and ocular		
CC	disorders. The polypeptides can also be used to aid wound healing and		
CC	epithelial cell proliferation, to prevent skin aging due to sunburn, to		
CC	maintain organs before transplantation, for supporting cell culture of		
CC	primary tissues, to regenerate tissues and in chemotaxis. The		
CC	polypeptides can also be used as a food additive or preservative to		

CC	increase or decrease storage capabilities. AAC93355 to AAC93363 and
CC	AAB51619 represent sequences which are used in the exemplification of the
CC	present invention
XX	
XX	Sequence 324 AA;
Query Match	70.9%; Score 1232; DB 3; Length 324;
Best Local Similarity	73.0%; Pred. No. 9.9e-122;
Matches 251; Conservative 10; Mismatches 41; Indels 42; Gaps 6;	
Qy	4 MELSAFSGQRTLLSAILSMLSLSPSTTSLLSNWFVGTOVKPKLCEKGLAACCPMPV 63
Db	1 MELSKAFSGQRTLLSAILSMLSLSPSTTSLLSNWFVGTOVKPKLCEKGLAACCPMPV 60
Qy	64 SLDDPTNTSTGEVVOYNWETGDDRFSPFRSGMWLSCEETVEBGERCRSPLETTPAK 123
Db	61 SLDDPTNTSTGEVVOYNWETGDDRFSPFRSGMWLSCEETVEBGERCRSPLETTPAK 120
Qy	124 REILMLSLGTQITTYIGLOFISFLLLDLLITGNPACGLKLSAPAAVSVLSGL----- 178
Db	121 RENPMVLPG-NADILHRTSIHQLEPPATNRLATINAEPC-----LMAQTERLCCEGFLCPVRS 174
Qy	179 -GWAHAMWISQVFOATYNLGPEDRPRHYMYNGAFYV-----AMISPT-----CC 222
Db	175 PGDAHAMWISQVFOATYNLGPEDRPRHYMYNGAFYVACSPSXAAMRRLSPKSTYTPGWC 234
Qy	223 MASAVTTENTYTRMWLEFCKHSGSKSPKENDPCLPHHHQCEPPRLSSAAPTGVPLTSYHOY 282
Db	235 MSSSAASIV-----KSPFENRNCPLPHHHQCEPPRLSSAAPTGVPLTSYHOY 279
Qy	283 HNQPIHVSSEGVDPFYSILRNKGFORGASQELKEAVRSSVEBQC 326
Db	280 HNQPIHVSSEGVDPFYSILRNKGFORGASQELKEAVRSSVEBQC 323
RESULT 14	
ABB89807	
ID	ABB89807 standard; protein; 330 AA.
AC	ABB89807;
XX	
DT	24-MAY-2002 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 2183.
XX	
KW	Cycostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW	vulnerant; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX	neurological disease; infection; human; secreted protein.
XX	
OS	Homo sapiens.
XX	
PN	WO200190304-A2.
XX	
PD	29-NOV-2001.
XX	
PP	18-MAY-2001; 2001MO-US016450.
XX	
PR	19-MAY-2000; 2000US-0205515P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Birse CB, Rosen CA;
XX	
DR	WPI; 2002-122018/16.
XX	
DR	N-PSDB; ABL90216.
XX	
PT	Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT	prevention of neural, immune system, muscular, reproductive,
PT	gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT	disorders.
XX	

PS Claim 11; SEQ ID NO 2183; 2081bp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AB089449-AB09085) and proteins
CC (AB089449-AB090444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC (e) neurological diseases such as cerebral ischaemia; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 330 AA;
Query Match 62.5%; Score 1086; DB 5; Length 330;
Best Local Similarity 98.5%; Pred. No. 3.3e-106;
Matches 201; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 123 KREILMLSGTQITTYIGLOPISFLILLTLTLGNPACGKLSAPFAVSSVSLGLGMYA 182
DB 127 KREILMLSGTQITTYIGLOPISFLILLTLTLGNPACGKLSAPFAVSSVSLGLGMYA 186
QY 183 HMYNSQVPAATVNLGPEDRPHVMNYGMAFYAMLSFTCCMASAVTTFNTYTRMVLKFC 242
DB 187 HMYNSQVPAATVNLGPEDRPHVMNYGMAFYAMLSFTCCMASAVTTFNTYTRMVLKFC 246
QY 243 KSKSKFENPNCIPHHOCFPRRLSSAAPTGVPLTSYHQNOPHISVSEGVDFYSELN 302
DB 247 KSKSKFENPNCIPHHOCFPRRLSSAAPTGVPLTSYHQNOPHISVSEGVDFYSELN 306
QY 303 KGFORGASQELKEAVRSSVEEBC 326
DB 307 KGFORGASQELKEAVRSSVEEBC 330
RESULT 15
AAM93674
ID AAM93674 standard; protein; 343 AA.
XX
AC AAM93674;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 3562.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000BP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
XX
PR 11-JAN-2000; 2000JP-0018774.
XX
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Ieogai T, Hayashi K, Ishii S, Kawai Y,
XX
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H,
XX
DR WPI; 2001-524255/58.

DR N-PSDB; AAK94609.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX
XX Claim 8; SEQ ID NO 3562; 1380bp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 343 AA;
Query Match 56.8%; Score 987.5; DB 4; Length 343;
Best Local Similarity 61.9%; Pred. No. 1e-95;
Matches 226; Conservative 13; Mismatches 65; Indels 61; Gaps 13;
QY 1 MAKXELSAFSGQRTLSAIIISMLSTSTSLSNVYFGVQKPKLCEKGLAAKGF 60
DB 1 MAKXELSAFSGQRTLSAIIISMLSTSTSLSNVYFGVQKPKLCEKGLAAKGF 60
QY 61 MPVSLDGDNTSTQEVQYNNMETGDRFSPRSFSGMWLSCETVEBBERCPSFIELTP 120
DB 61 MPVSLDGDNTSTQEVQYNNMETGDRFSPRSFSGMWLSCETVEBBERCPSFIELTP 120
QY 121 PAKREKELGL-----LEFATLQGPCHPTLRG-----GKRIMEKASLPSPPGLGCK 179
DB 121 PAKREKELGL-----LEFATLQGPCHPTLRG-----GKRIMEKASLPSPPGLGCK 166
QY 180 ---MVA-----HMYNSQVPO---ATVNLGPEDRPHVMNYGMAFYAMLSFTCCMASAVTT 229
DB 167 NPMVLPGNADHLARSTHQLPPATRLATH-WEPCLM-----AQTRLLCCCFCPYRS 218
QY 230 -----FNTYTRMV-----LEFKC-----KSKSK---FKENPNC---LPH-HHQC 261
DB 219 PGDGGPHVFTSLPBDCCQSGSRLETTCLLEMLGILLHALLHLHGVGCHHLQVHHQC 278
QY 262 FPRRLSSAAPTGVPLTSYHQNOPHISVSEGVDFYSELNKGFGORGASQELKEAVRSSV 321
DB 279 FPRRLSSAAPTGVPLTSYHQNOPHISVSEGVDFYSELNKGFGORGASQELKEAVRSSV 338
QY 322 EEEBC 326
DB 339 EEEBC 343

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Job time : 111.417 secs

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OM protein - protein search, using sw model

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Title: US-10-019-151C-3

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Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1725	99.3	339	US-09-729-674-138	Sequence 138, App
2	1725	99.3	339	US-10-913-553-138	Sequence 138, App
3	1086	62.5	330	US-10-264-237-2183	Sequence 2183, App
4	657.5	37.8	285	US-09-989-722-272	Sequence 272, App
5	657.5	37.8	285	US-09-989-723-272	Sequence 272, App
6	657.5	37.8	285	US-09-989-729-272	Sequence 272, App
7	657.5	37.8	285	US-09-989-727-272	Sequence 272, App
8	657.5	37.8	285	US-09-989-731-272	Sequence 272, App
9	657.5	37.8	285	US-09-989-732-272	Sequence 272, App
10	657.5	37.8	285	US-09-991-073-272	Sequence 272, App
11	657.5	37.8	285	US-09-990-442-272	Sequence 272, App

12	657.5	37.8	285	US-09-991-163-272	Sequence 272, App
13	657.5	37.8	285	US-09-993-604-272	Sequence 272, App
14	657.5	37.8	285	US-09-990-456-272	Sequence 272, App
15	657.5	37.8	285	US-09-989-721-272	Sequence 272, App
16	657.5	37.8	285	US-09-992-598-272	Sequence 272, App
17	657.5	37.8	285	US-09-989-293A-272	Sequence 272, App
18	657.5	37.8	285	US-09-989-735-272	Sequence 272, App
19	657.5	37.8	285	US-09-990-444-272	Sequence 272, App
20	657.5	37.8	285	US-09-991-181-272	Sequence 272, App
21	657.5	37.8	285	US-09-989-730-272	Sequence 272, App
22	657.5	37.8	285	US-09-990-436-272	Sequence 272, App
23	657.5	37.8	285	US-09-993-687-272	Sequence 272, App
24	657.5	37.8	285	US-09-989-734-272	Sequence 272, App
25	657.5	37.8	285	US-09-997-653-272	Sequence 272, App
26	657.5	37.8	285	US-09-989-724-272	Sequence 272, App
27	657.5	37.8	285	US-09-989-728-272	Sequence 272, App
28	657.5	37.8	285	US-09-990-441-272	Sequence 272, App
29	657.5	37.8	285	US-09-993-667-272	Sequence 272, App
30	657.5	37.8	285	US-09-997-428-272	Sequence 272, App
31	657.5	37.8	285	US-09-997-666-272	Sequence 272, App
32	657.5	37.8	285	US-09-990-438-272	Sequence 272, App
33	657.5	37.8	285	US-09-990-562-272	Sequence 272, App
34	657.5	37.8	285	US-09-990-711-272	Sequence 272, App
35	657.5	37.8	285	US-09-989-726-272	Sequence 272, App
36	657.5	37.8	285	US-09-998-156-272	Sequence 272, App
37	657.5	37.8	285	US-09-990-437-272	Sequence 272, App
38	657.5	37.8	285	US-09-991-157-272	Sequence 272, App
39	657.5	37.8	285	US-09-997-514-272	Sequence 272, App
40	657.5	37.8	285	US-09-997-573-272	Sequence 272, App
41	657.5	37.8	285	US-09-991-172-272	Sequence 272, App
42	657.5	37.8	285	US-09-990-726-272	Sequence 272, App
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45	657.5	37.8	285	US-09-990-443-272	Sequence 272, App

ALIGNMENTS

RESULT 1
US-09-729-674-138
Sequence 138, Application US/09729674
Patent No. US20010039335A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Byrne, Cheryl
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steindinger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Rehtel, Kim
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729, 674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539, 330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 138
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-729-674-138
Query Match 99.3%; Score 1725; DB 9; Length 339;

Best Local Similarity 99.7%; Pred. No. 1,6e-173;
Matches 333; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHELSTAFSGQRTLLSAILSMLSLSPSTTSLSNVYFVGTQVKKPLCEKGLAAKCFDMP 62
DB 16 EHELSTAFSGQRTLLSAILSMLSLSPSTTSLSNVYFVGTQVKKPLCEKGLAAKCFDMP 75
QY 63 VSLDGTNTSTQEVVQYNNMETGDDRFSPFSFGSMWLSCEETVEEGERCRSPFIELTPPA 122
DB 76 VSLDGTNTSTQEVVQYNNMETGDDRFSPFSFGSMWLSCEETVEEGERCRSPFIELTPPA 135
QY 123 KHEILMLSLGTQITTYIGLQFISFLILLTLTGNPACGLKLSAFAVSSVLSGLGMVA 182
DB 136 KHEILMLSLGTQITTYIGLQFISFLILLTLTGNPACGLKLSAFAVSSVLSGLGMVA 195
QY 183 HMYSQVFQATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLFFKC 242
DB 196 HMYSQVFQATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLFFKC 255
QY 243 KHSKSPKENPCLPHHQCFFPRLSSAAPTVGPLTSYQYHNPPIHSVSEGVDFYSELRN 302
DB 256 KHSKSPKENPCLPHHQCFFPRLSSAAPTVGPLTSYQYHNPPIHSVSEGVDFYSELRN 315
QY 303 KGFQASQELKEAVRSSVVEEQC 326
DB 316 KGFQASQELKEAVRSSVVEEQC 339

RESULT 2
US-10-913-553-138
; Sequence 138, Application US/10913553
; Publication No. US20050003491A1
GENERAL INFORMATION:
; APPLICANT: Jacobo, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavalie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinhinger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fectel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/10/913,553
; PRIOR APPLICATION NUMBER: US/09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 138
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-913-553-138

Query Match 99.3%; Score 1725; DB 17; Length 339;
Best Local Similarity 99.7%; Pred. No. 1,6e-173;
Matches 333; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KHELSTAFSGQRTLLSAILSMLSLSPSTTSLSNVYFVGTQVKKPLCEKGLAAKCFDMP 62
DB 16 EHELSTAFSGQRTLLSAILSMLSLSPSTTSLSNVYFVGTQVKKPLCEKGLAAKCFDMP 75
QY 63 VSLDGTNTSTQEVVQYNNMETGDDRFSPFSFGSMWLSCEETVEEGERCRSPFIELTPPA 122
DB 76 VSLDGTNTSTQEVVQYNNMETGDDRFSPFSFGSMWLSCEETVEEGERCRSPFIELTPPA 135

QY 123 KHEILMLSLGTQITTYIGLQFISFLILLTLTGNPACGLKLSAFAVSSVLSGLGMVA 182
DB 136 KHEILMLSLGTQITTYIGLQFISFLILLTLTGNPACGLKLSAFAVSSVLSGLGMVA 195
QY 183 HMYSQVFQATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLFFKC 242
DB 196 HMYSQVFQATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLFFKC 255
QY 243 KHSKSPKENPCLPHHQCFFPRLSSAAPTVGPLTSYQYHNPPIHSVSEGVDFYSELRN 302
DB 256 KHSKSPKENPCLPHHQCFFPRLSSAAPTVGPLTSYQYHNPPIHSVSEGVDFYSELRN 315
QY 303 KGFQASQELKEAVRSSVVEEQC 326
DB 316 KGFQASQELKEAVRSSVVEEQC 339

RESULT 3
US-10-264-237-2183
; Sequence 2183, Application US/10264237
; Publication No. US20040009491A1
GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4131p1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2183
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2183

Query Match 62.5%; Score 1086; DB 15; Length 330;
Best Local Similarity 98.5%; Pred. No. 6,9e-106;
Matches 201; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 123 KHEILMLSLGTQITTYIGLQFISFLILLTLTGNPACGLKLSAFAVSSVLSGLGMVA 182
DB 127 KHEILMLSLGTQITTYIGLQFISFLILLTLTGNPACGLKLSAFAVSSVLSGLGMVA 186
QY 183 HMYSQVFQATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLFFKC 242
DB 187 HMYSQVFQATVNLGPEDMRPHVMNYGMAFYMAWLSFTCCMASAVTTFTNTYTRMVLFFKC 246
QY 243 KHSKSPKENPCLPHHQCFFPRLSSAAPTVGPLTSYQYHNPPIHSVSEGVDFYSELRN 302
DB 247 KHSKSPKENPCLPHHQCFFPRLSSAAPTVGPLTSYQYHNPPIHSVSEGVDFYSELRN 306
QY 303 KGFQASQELKEAVRSSVVEEQC 326
DB 307 KGFQASQELKEAVRSSVVEEQC 330

RESULT 4
US-09-989-722-272
; Sequence 272, Application US/09989722
; Patent No. US20020072067A1
GENERAL INFORMATION:
; APPLICANT: Aehkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter

APPLICANT: Gertlesen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: KJavain, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Metcane, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472

;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
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;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;
Best Local Similarity 51.6%; Pred. No. 1.3e-60;
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

QY 1 MAMMELSKAFSGQRTLLSAILSMLSLSPFTTSLSNVWVGQKVPKPLCEKGLAAKCPD 60
DB 1 MAMMELSKAFSGQRTLLSAILSMLSLSPFTTSLSNVWVGQKVPKPLCEKGLAAKCPD 60
QY 61 MPVSLGDDTNTSTQEVYVQVWMTGDDRFPSFRSGMWLSCERTVBSFGRCSTFIETLP 120
DB 61 MPVSLGDDTNTSTQEVYVQVWMTGDDRFPSFRSGMWLSCERTVBSFGRCSTFIETLP 120
QY 121 PAKRBILMISLGIQTYIGLOPISFLILLTDLLTGPAQGLLSAFAAVSVLSGLIG- 179
DB 121 PAKRBILMISLGIQTYIGLOPISFLILLTDLLTGPAQGLLSAFAAVSVLSGLIG- 179
QY 180 --MVA-----HMVYQVQFQ---ATVNLGPEDMRPHVWNYGMATYMWLSPFCMASAVTT 229
DB 167 NPVAVIGNDHMLHRTSIHQLPATNRLATN-WEPCLM-----AQTRBLGCC----- 211
QY 230 FNTYTTMVLTFKCKHKSFKENPN---CLPHHQCPRRLSAA-----PTVGLPSTYH 280
DB 212 -----FLCPVNSPDGSGPHDVFTSLPSDCQLSRRLFTTCELEMTGLHGLALH 261
QY 281 Q-----YHNPRIHSVSEGV 294
DB 262 LHHGVGCHHLQHVHODGAGV 281

RESULT 5
US-09-989-723-272
;; Sequence 272, Application US/09989723
;; Patent No. US20020072092A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Geider, Hanspeter
;; APPLICANT: Gerlitsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Guiney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PLC62
;; CURRENT APPLICATION NUMBER: US/09/989,723
;; PRIOR FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/06770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE:	1998-06-04
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PRIOR FILING DATE:	1998-06-23

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2	PRIOR FILING DATE: 1998-06-23
3	PRIOR APPLICATION NUMBER: 60/0904299
4	PRIOR FILING DATE: 1998-06-24
5	PRIOR APPLICATION NUMBER: 60/0904311
6	PRIOR FILING DATE: 1998-06-24
7	PRIOR APPLICATION NUMBER: 60/0904355
8	PRIOR FILING DATE: 1998-06-24
9	PRIOR APPLICATION NUMBER: 60/0904444
10	PRIOR FILING DATE: 1998-06-24
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12	PRIOR FILING DATE: 1998-06-24
13	PRIOR APPLICATION NUMBER: 60/0904772
14	PRIOR FILING DATE: 1998-06-24
15	PRIOR APPLICATION NUMBER: 60/0905535
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47	PRIOR APPLICATION NUMBER: 60/0916266
48	PRIOR FILING DATE: 1998-07-02
49	PRIOR APPLICATION NUMBER: 60/0916333
50	PRIOR FILING DATE: 1998-07-02
51	PRIOR APPLICATION NUMBER: 60/0919788
52	PRIOR FILING DATE: 1998-07-07
53	PRIOR APPLICATION NUMBER: 60/0919882
54	PRIOR FILING DATE: 1998-07-07
55	PRIOR APPLICATION NUMBER: 60/0921882
56	PRIOR FILING DATE: 1998-07-09

Query Match	37.8%;	Score 657.5;	DB 9;	Length 285;
Best Local Similarity	51.6%;	Pred. NO. 1.3e-60;		
Matches 165; Conservative	14;	Mismatches 76;	Indels 65;	Gaps 11;

Qy	1	MAKHELSKASGORTLSALISMUSLSPSTLSLSNWPQCTOKVPRDLCEKJLAAACFD	60
Db	1	MAKHELSKASGORTLSALISMUSLSPSTLSLSNWPQCTOKVPRDLCEKJLAAACFD	60
Qy	61	MPVSLDDDTNSTOEVVQYNNMETGDDRFRRSPFSGMNLSCBETVEBBERCRSFISLTP	120
Db	61	MPVSLDDDTNSTOEVVQYNNMETGDDRFRRSPFSGMNLSCBETVEBBERCRSFISLTP	120
Qy	121	PAKKEIIMLSAGTOITYIGHQPIFSFLILLTDLLLTGHPACGLKLSAAVAASVSLGILG-	179
Db	121	PAKKEIKGL-----LEPALLQCPCHPTLRFG-----GKRLMERKASLPSPELJGCGK	166

[illegible]

PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;
Best Local Similarity 51.6%; Pred. No. 1,36-60;
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

Qy 1 MARKELSKAFSGQRTLLSAILLSMLSLSPSTTSLSNWPGTQVNPRLCEKGIACPCD 60
Db 1 MARKELSKAFSGQRTLLSAILLSMLSLSPSTTSLSNWPGTQVNPRLCEKGIACPCD 60
Qy 61 MPVSLDDDTNTSTQEVQVQWMMENGDPRFSPRSGMWLSCETVVEPGRCRSFIILTP 120
Db 61 MPVSLDDDTNTSTQEVQVQWMMENGDPRFSPRSGMWLSCETVVEPGRCRSFIILTP 120
Qy 121 PAKREILMSLGTQITTYIGLQFISFLLLLTDLLLTGNPACGLKLSAPAAVSVLSGLG- 179
Db 121 PAKRGEKGL-----LEPATLQGPCHPTLRFG-----GKRLMERKASLPSPLGCGK 166
Qy 180 --MYA-----HMTSQVQFQ---ATVNLGPEDMRPHVNYNGAFYMAVLSFTCCMAAVTT 229
Db 167 NPWVTPGNADHLHRTSHQLEPPATNRLATN-WEPCIM-----AQTERLCCC----- 211
Qy 230 FNTYTRVNLBPKGHSFKENPN-----CLPHHQCPRLSSAA-----PTVGPLTSYH 280
Db 212 -----FLCPVNSPGDGGPHDVFTSLPSDCQLGSRRLBETTCLEMLGILGLALLH 261
Qy 281 Q-----YHNPPIHSVSGV 294
Db 262 LMGVGHLLQHYHQDQAGV 281

RESULT 7
US-09-989-727-272
Sequence 272, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Batton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumaas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;
Best Local Similarity 51.6%; Pred. No. 1.3e-60;
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

QY 1 MARKELSKAFSGQTTLSAISMSTLSSTTSLSNVFTQYKPPKLGIAACFD 60
DB 1 MARKELSKAFSGQTTLSAISMSTLSSTTSLSNVFTQYKPPKLGIAACFD 60

QY 61 MPVSLDDGTNTSTQVQYVNWETGDDRRSPRSGMWLSCBETVBERGRCRSPILTP 120
DB 61 MPVSLDDGTNTSTQVQYVNWETGDDRRSPRSGMWLSCBETVBERGRCRSPILTP 120

QY 121 PAKKELIWLSTGTOITYIGLQFISPLLLTDLTLTGNPACGLKLAPAAVSSVLGLG- 179
DB 121 PAKKGEKGL-----LEFATLQGPCHPTLRF-----GKRLMEKASLSPPLGCGK 166

QY 180 --WVA-----HMRTSQVFQ--ATVNTGPEWRPHVWNYGAFYMANLSFTCCMASAVTT 229
DB 167 NPWVLPGNADHHTSTHQLPPTATRLATH-WBPCLW-----AOTERLCCC----- 211

QY 230 FNTYTRVNLBPKCKHSGHSFKENRP-----CLPHHQCPRLSSAA-----PTVGPILSYH 280
DB 212 -----FLCPVRSPPGCGPRDVTSLSPSCQLSRRLTTCBLMTGLHGLMLH 261

QY 281 Q-----YHNPRIHSEGV 294
DB 262 LKHGVGCHLQHNVHQDQAGV 281

RESULT 8
US-09-989-731-272
Sequence 272, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: KJavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989, 731
CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; length 285;
Best local Similarity 51.6%; Pred. No. 1.3e-60;
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

QY 1 MAKMEISKAFSGORTLLSAILMSLSFSTTSLSNYVGTQKPKPLCEGLAKCPD 60
|||
DB 1 MAKMEISKAFSGORTLLSAILMSLSFSTTSLSNYVGTQKPKPLCEGLAKCPD 60

QY 61 MPVSLDGDNTSTQEVQVQNMETGDDRFSPFRSGMMVSCSEYEBPGERCRSFTELTP 120
|||
DB 61 MPVSLDGDNTSTQEVQVQNMETGDDRFSPFRSGMMVSCSEYEBPGERCRSFTELTP 120

QY 121 PAKRBLMLSLGTQYTYIGLQPIISPLLLTDLTLGNPACGKLKSAFAVSSVLGSLG- 179
|||
DB 121 PAKRGEKGL-----LEFATLQGPCHPLTRFG---GRMLKKSLSPPPLGLGCK 166

QY 180 --MVA-----IMMYSOVFO--ATYNLGPEDMRPHVNYGMAFYMAWLSFTCCMASAVTT 229
|||
DB 167 NPMVIFGNADHLHRISIHQIPRATNRLATH-WEPCLM-----AQTERLCCC----- 211

QY 230 FNTYTRMVLFPCKSKSKSPKENPN-----CLPHHOCFPRRLSSAA-----PTVGPPLYTH 280
|||
DB 212 -----FLCPVRSPDGGPHDVFYSLSBDCQUGSRRLTTCLEMLGLHLGLALH 261

QY 281 Q-----YHNPRIHVSSEGV 294
|||
DB 262 LHHGVGCHHLQHVHODGAGV 281

RESULT 9
US-09-989-732-272
; Sequence 272, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
FILE REFERENCE: P2730P1C57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09
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Query Match      37.8%; Score 657.5; DB 9; Length 285;
Best Local Similarity 51.6%; Pred. No. 1.3e-60;
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;
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DB      61 MPMVSLDGDNTSTQEVVQNMWEGDGRFSPSPRSGMMLSCETVBEPEBCRSFIELTP 120
QY      121 PAKREIIMLSGTQTYIGLOFISFLLTLDTLLTGNPACGLKLSFAVSSVLSGLG- 179
DB      121 PAKRGEKGL-----LEFATLOGRCHPTLRFG---GKRLMEKALPBPRLGLCSK 166
QY      180 --MVA---HMYSQVFG--ATVNLGSDMRPHVWNYGMARFYAMWLSFTCCMASAVTT 229
DB      167 NPMVLPGNADHLRHSIHQLPRATNMLATN-WERPCIL-----AQTERLCCC----- 211
QY      230 FMTYTRMVLBFKCKSKSKSPKENDN-----CLRNHQCFRRRLSSAA-----PYVGRYLSYH 280
DB      212 -----FLCVRVRSPEDDGGRHDVFTSLPSDCQJGSRRLTTCLELMLGLLHGLALLH 261
QY      281 Q-----YANOPRHSVSEGV 294
DB      262 LHHGVCCHLQNVHNDQDAGV 281
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RESULT 10
US-09-991-073-272
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/ Sequence 272, Application US/09991073
/ Patent No. US20020127576A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
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/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Geider, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Guiney, Auelin L.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730PIC15
/ CURRENT APPLICATION NUMBER: US/09/991,073
/ PRIOR FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/049787
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;
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 Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

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RESULT 11
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; Sequence 272, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C8
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; PRIOR FILING DATE: 1998-07-09
Query Match      37.8%; Score 657.5; DB 9; Length 285;
Best Local Similarity 51.6%; Pred. No. 1,36-60;
Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

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DB 1 MAKWELSKAVSGORTLSLISLMSLSLSPSTTSLSNWPGTQVPPYLCCKGLAACPD 60
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RESULT 13
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; Sequence 272, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Aekhenazi, Av1 J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grunwald, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
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; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;
Best Local Similarity 51.6%; Pred. No. 1,3e-60;

Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

QY 1 MAKMEISKAFSGQRTLLSAHLSMLSLFSTTSLSNYFVGTQYKPKLCEKGLAKCPD 60
DB 1 MAKMEISKAFSGQRTLLSAHLSMLSLFSTTSLSNYFVGTQYKPKLCEKGLAKCPD 60
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DB 61 MPVSLDGTNTSTQBVQYNNMETGDDRFPSFRSGMWLSCEETVEBBERCRSFTELTTP 120
QY 121 PAKREILMUSLGTQYTYIGLOPISFLLLTDLTLGNPACGKJASAPAAVSVLSGLLG- 179
DB 121 PAKREILMUSLGTQYTYIGLOPISFLLLTDLTLGNPACGKJASAPAAVSVLSGLLG- 179
QY 121 PAKREILMUSLGTQYTYIGLOPISFLLLTDLTLGNPACGKJASAPAAVSVLSGLLG- 166
DB 121 PAKREILMUSLGTQYTYIGLOPISFLLLTDLTLGNPACGKJASAPAAVSVLSGLLG- 166
QY 180 --MVA-----HMVSGVFO--ATVNLGPEDEWRPHVWYGMFAFYAMLSFTCCMASAVTT 229
DB 167 NEMVLPGNADHHRISHQIPATYRLATH-WEPCW-----AQBERLCCC----- 211
QY 230 FNTYTRMVLFEKCKSKSPKENPN---CLPHHQCFFRRLSAA-----PTVGPSTYH 280
DB 212 -----FLCPVRSPDGGPHDVFTSLPDCQLGSRRLRTTCLBLWLGHLGIALHL 261
QY 281 Q-----YHNPPIHSVSEGV 294
DB 262 LILHGVGCHLQHVHODGAGV 281

RESULT 14
; Sequence 272, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Aabkenazi, Avi J.
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC22
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PRIOR FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
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RESULT 15

; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Bobcelli, David

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Godowski, Paul J.

1 APPLICANT: Grimaldi, J Christopher
 2 APPLICANT: Gurney, Austin L.
 3 APPLICANT: Kijavini, Ivar J.
 4 APPLICANT: Napier, Mary A.
 5 APPLICANT: Pan, James
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 7 APPLICANT: Roy, Margaret Ann
 8 APPLICANT: Stewart, Timothy A.
 9 APPLICANT: Tuma, Daniel
 10 APPLICANT: Watanabe, Colin K.
 11 APPLICANT: Williams, P. Mickey
 12 APPLICANT: Wood, William I.
 13 APPLICANT: Zhang, Zemin
 14 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 15 TITLE OF INVENTION: Acids Encoding the Same
 16 FILE REFERENCE: P2730P1C55
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 PRIOR FILING DATE: 1998-07-09

Query Match 37.8%; Score 657.5; DB 9; Length 285;
 Best Local Similarity 51.6%; Pred. No. 1.3e-60;
 Matches 165; Conservative 14; Mismatches 76; Indels 65; Gaps 11;
 QY 1 MANBELSKAFSGORTLSAITSLSFSTLSNMYWVGTOVKRPLCEKGLAKCPD 60
 1 MANBELSKAFSGORTLSAITSLSFSTLSNMYWVGTOVKRPLCEKGLAKCPD 60
 QY 61 MPVSLDGDNTSTQEVYQVNMETGDRFSFRSGMWLSCERTVEBPGRCRSTFLTP 120
 61 MPVSLDGDNTSTQEVYQVNMETGDRFSFRSGMWLSCERTVEBPGRCRSTFLTP 120
 QY 121 PAKREILWLSLGTQIYIGQPIFLLLDLTJONPACGLKSAFANVSVLSGLG- 179
 121 PAKREILWLSLGTQIYIGQPIFLLLDLTJONPACGLKSAFANVSVLSGLG- 179
 QY 180 --MVA-----HMVYSGVFO---ATVNIAGPEWREPHVYNYGMAYMAMLSFTCCMASAVTT 229
 180 --MVA-----HMVYSGVFO---ATVNIAGPEWREPHVYNYGMAYMAMLSFTCCMASAVTT 229
 QY 167 NPWVIRGNNDHLHRTSHIQLPATNRLATN-WEPCLM-----AQTERLCCC----- 211
 167 NPWVIRGNNDHLHRTSHIQLPATNRLATN-WEPCLM-----AQTERLCCC----- 211
 QY 230 FNTYTMVLEPFCKKSKSKSKRENPN---CLPHHQCFFPRRLSAA-----PTVGPILTSYH 280
 230 FNTYTMVLEPFCKKSKSKSKRENPN---CLPHHQCFFPRRLSAA-----PTVGPILTSYH 280
 QY 281 Q-----YANOPHSVSEGV 294
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 QY 262 LKHGVCCHLQYVHDQAGV 281
 262 LKHGVCCHLQYVHDQAGV 281

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 Job time : 102.919 secs

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Biochem. Biophys. Res. Commun. 262, 103-108, 1999
A:Title: Molecular characterization of the first heat shock protein 70 from a reef coral
A:Reference number: JCT088; PMID:99382249; PMID:10448076
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A:Gene: hsp70
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C:Keywords: ATP; molecular chaperone

Query Match
Best Local Similarity 26.8%; Pred. No. 0.34;
Matches 33; Conservative 11; Mismatches 42; Indels 37; Gaps 3;

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DB 219 FFOVLSTAGNTHLGSEDFDKRMVDY-----FVSDPKCK 251

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DB 252 HKKDLKTNPKSL-----RLKTKACERAKKTLSSNSQANVEIDSLFEGIDFYSLRTTRA 303

QY 304 GFG 306
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RESULT 3
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C:Accession: H84698
R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bent, M.T.; Town, C.D.; Fujii, C.Y.;
M. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vaitaken, S.E.; Umayam, L.; Talbot, L.;
Eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; PMID:20083487; PMID:10617197
A:Accession: H84698
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <STO>
A:Cross-references: UNIPROT:O82390; GB:AB020293; NID:g3582333; PIDN:AAAC35230.1; GSPDB:GN
C:Genetics:
A:Gene: At2g29650
A:Map position: 2
C:Superfamily: hexuronate transporter

Query Match
Best Local Similarity 20.6%; Pred. No. 0.84;
Matches 63; Conservative 41; Mismatches 100; Indels 102; Gaps 16;

QY 26 LSPSTSLSNVYFGTQKPKP-----LCEKGLAKCP-----MFVSLDGTNTS 72
DB 84 VSDSPSISVLPWM-----EEPPKRWVTLCLFSAFLCNDNRVNMISAILFMSAEYGMNPA 139

QY 73 TGVVVOYNNMETGDRFSFRSFGMWLSCEITVBBGERCRSLTLPRAKRIILWLSIG 132
DB 140 TGLIIOSSFFWG--YLLTIOAGIIV--ADTV--GGRKVLGP-----GVIMWSIA 182

QY 133 TQITTYIGLQF--ISFLLLTDLTLTGN-----PACGLKLSAPAAVSS-----VLSGI-LG 179
DB 183 TITTPAAKLGILYLLVRAFMGVGSGVAMPAAMNIIISKVPPQBSRSLSALVYSGWYLG 242

QY 180 MVAHMYISQVFOATVNIGPDMRPHVWNYGM--AFY-----MAWLSFTCCMAASAVTTEN 231
DB 243 SYTGIAFSFPL-----IHQFGMPSVFYSFGSLGTVMVTL----- 276

QY 232 TYTRMWLEPKCKHKSFKENPNCPLPHH-----OCPPRLSSAAPTGVPLTS 278
DB 277 -----ILTAAESSPLEDPILLPEERKLIADNCASKSPKVSIPWRLTILSKPWALLS 328

QY 279 YHQYHN 284
DB 329 CHFCN 334

RESULT 4
B45871
dnaK-type molecular chaperone HSP70-Hom - human
N:Alternate names: heat shock protein HSP70-Hom
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 03-Jul-2004
C:Accession: B45871
R:Miller, C.M.; Campbell, R.D.
Immunogenetics 32, 242-251, 1990
A:Title: Structure and expression of the three hrc-linked HSP70 genes.
A:Reference number: A45871; PMID:91055806; PMID:1700760
A:Accession: B45871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-641 <ML>
A:Cross-references: UNIPROT:P34931; GB:M59829; GB:M34268; NID:g188491; PIDN:AAA63228.1;
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein compl
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match
Best Local Similarity 27.7%; Pred. No. 1.5;
Matches 26; Conservative 15; Mismatches 38; Indels 15; Gaps 2;

QY 234 TRMWLEPKCKHKSFKENPNCPLPHHOCPPRLSSAAPTGVPLTSHYQHNQPIHSVSEG 293
DB 241 SHFVEFKCKHKKKIDISQNRVAV-----RLRACERAKKTLSSSTQANLEIDSLYEG 292

QY 294 VDFYSELKNGKFGQ-----RGASQELKAVVSS 320
DB 293 IDFTYSITRAREBELCADLFGTLBPEVALRDA 326

RESULT 5
S41415
dnaK-type molecular chaperone Hsp70.3 - rat
N:Alternate names: heat shock protein 70
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41415; I68987
R:Putz, W.
Submitted to the EMBL Data Library, January 1994
A:Reference number: S41415
A:Accession: S41415
A:Molecule type: DNA
A:Residues: 1-641 <LUT>
A:Cross-references: UNIPROT:P55063; EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:g450
Immunogenetics 40, 325-330, 1994
A:Title: Comparative analysis of the three major histocompatibility complex-linked heat
A:Reference number: I54542; PMID:95012453; PMID:7927536
A:Accession: I68987
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-641 <RES>
A:Cross-references: EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:g450934
C:Genetics:
A:Gene: hsp70-3
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein compl
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

```

Query Match      5.3%; Score 92.5; DB 2; Length 641;
Best Local Similarity 26.6%; Pred. No. 1.9;
Matches 25; Conservative 17; Mismatches 37; Indels 15; Gaps 2;

QY      234 TRNVLEPKCKHSFKENPNCLPHNHOCFRRLLSNAAPVGLTSTYOHYNOPHSVSEG 293
      : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      241 SHFEVEFKRKHKQKQKQISQNKRAV-----RLATACERAKRTLSSTQANLEIDSLYEG 292
      : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      294 VDFVSELRNKGPO-----RGASQELKAVVSS 320
      : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      293 IDFTTSTTRARFELCADLFRGTLPEVEKSLDA 326
      : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
S74477
hypothetical protein slr1114 - Synechocystis sp. (strain PCC 6803)
C|Species: Synechocystis sp.
A|Variety: PCC 6803 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C|Date: 25-Apr-1997
C|Accession: S74477
R|Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, K.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A|Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S74477
A|Reference number: S74322; MUID:97061201; PMID:8905231
A|Accession: S74477
A|Status: nucleic acid sequence not shown; translation not shown
A|Molecule type: DNA
A|Residues: 1-585 <KAN>
A|Cross-references: UNIPROT:P7627, EMBL:D90899, GB:AB001339, NID:G1651650, PIDD:BA16627
A|Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C|Superfamily: Synechocystis hypothetical protein slr1114

```

Query Match	5.3%	Score 92	DB 2	Length 589
Best Local Similarity	22.3%	Pred. No. 1.9		
Matches	58	Mismatches	92	Indels 70
		Gaps	14	
QY	5	ELSKAFSGQRT---	LSAISLMSLSSTTSLSNWFGTQKPKLCEKG--	LAACK 58
DB	22	ELKSFRTATKRWMLLVSVIFQGVWVFRT-----	SRIPVLYLNLNAGEGQFSRYXC	71
QY	59	FDMPFLSLGDYNN--TSTQEV--	VOYNNET--GDDEFSRSPR-----	SGMWLSCEBTV 105
DB	72	LSTPDPWYKSGIRPCTQDLDLQGLINRWMLDQFALSLAGLALLVAGVYLLVADLQ		131
QY	106	EEPERGCRSPFELTPPARBEILM-----	LSLGTQTYIGLOPIS-----	PLLLITD 151
DB	132	KECGRTGLNFTRLSPQGGNFIWGMGLGVPSILYGFLLTLLPLHIVAAAGAGISILLIING		191
QY	152	---LLLTG---NDCGLKLSAFA---	AVSSVLSGLGGMVAHMYSGVFQATVNLGP	198
DB	192	YVAVVLNAGATPFPHIALMIGLSSNNKYSLSKSAIADLCGV-----	GLIATITLIMQD	245
QY	199	EDMRPHVWNYGAPFMATNIS	218	
DB	246	NDMEP-----	PFLSWLS	257

```

RESULT 7
T45468
dnaK-type molecular chaperone Hsp70 [imported] - bloodfluke planorb
N:Alternate names: heat shock protein 70
C:Species: Biomphalaria glabrata (bloodfluke planorb)
C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C:Accession: T45468
R:Yoshino, T.P.; Wu, X.J.; Liu, H.D.
submitted to the EMBL Data Library, November 1997
A:Description: transfection and heat-inducible expression of a molluscan promoter-luciferase reporter construct
A:Reference number: Z22978
A:Accession: T45468
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

```

A:Residues 1-636 <YOS>
A:Cross-references: UNIPROT:O44343; EMBL:AF025477; PDB:1ABB9911.1
A:Experimental source: strain PR albino
C:Genetics:
A:Gene: HSP70
C:Superfamily: heat shock protein 70

Query Match	5.3%	Score 91.5	DB 2	Length 636
Best Local Similarity	27.7%	Pred. No. 2.3		
Matches	26	Conservative	15	Mismatches 38
				Indels 15
				Gaps 2

```

Oy  23  TRAVLEKCHSXSFPENNCCLPHHOCPEPLTSAATVGPLTSYQHNPYHVSSEG  29
      ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  243  THRVGFPRKRYNMDSNPRL-----RLQIACRCARARTISSESSAIEIDSLYEG  294
Oy  294  VDFYSELKNGRPQ-----RCAGDELKAVNSS  320
      ||| ::| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  295  IDFYTKITRRAPFEELCGDLFRSTLDPVETALMDA  328

```

RESULT 8

hypothetical protein F10M10.30 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T04772
 C:Byeuan, M.; De Haan, M.; Maaree, A.C.; Griwell, L.A.; Hohelsel, J.; Mewes, H.W.; Mayer
 submitted to the Protein Sequence Database, February 1999
 A:Reference number: Z15384
 A:Accession: T04772
 A:Molecule type: DNA
 A:Residues: 1-847 <BEV>
 A:Cross-references: UNIPROT:Q9SYZ1; EMBL:AL035521
 A:Experimental source: cultivar Columbia; BAC clone F10M10
 A:Genetics:
 A:Map position: 4
 A:Introns: 91/1; 139/3; 416/1; 475/3; 528/3; 603/3; 663/1; 748/2
 A:Note: F10M10.30
 C:Superfamily: Arabidopsis thaliana hypothetical protein F10M10.30

Query Match	5.24	Score 91	DB 2	Length 847
Best Local Similarity	24.18	Pred. NO. 3.7		
Matches 66	Conservative 33	Mismatches 97	Indels 78	Gaps 16

```

QY      55 AAKCFPMPLSLGDN-----TSGEVQVNM-----EGDDRFSRSPSGMWL- 99
Db      303 ASBNFGEPTTMEVDISKIDPAKCVNRISVOKTISDLYARHLGDYKLRN-RVSIHLS 360
QY      100 --SCETVEE--PGERCRSPTEIIPAKREIL-----WISL-----GTQITYIGLOPIS 144
Db      361 GSSTNETVQOASTTAEKRVRSFKTDQDFELVIELFYQGYRILLSSRRPGTQVA--NIQ--A 416
QY      145 FILLITLITLL-----AGNPAGLKL-----SARA--AVSSV 173
Db      417 FVSLTPELLRLTYCGAPHLNINLOMYNTHSLPGNIRECOEPLFDYNSALAINGRKTAQV 476
QY      174 LSGLTGMVAHMYSCVQFQATVNLGPEBDIRPHVNYNG--MAFYAMLSPTCCMASAVTTEN 231
Db      477 NFGASGVMAHVQSDIWAKTSPDRGEAVVA--LMPMGAGMLCTHAMEHYTTMDKEFLKKK 534
QY      232 TY-----TRWLEPKCKHSKSF--KENNCLPPIH 258
Db      535 GTPLEGGCTSPLLDMLTNGKDGFLQTNSTSPBH 568

```

RESULT 9

dnaK-type molecular chaperone Hsc70c - mouse
 N/Alternate names: heat shock protein 70
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I49761
 C/Shook, M.; Olavsen, M.G.; van Vugt, H.; Milner, C.M.; Teuscher, C.; Campbell, R.D.

Immunogenetics 40, 159-162, 1994
 A:Title: Coding sequences and levels of expression of Hsc70c are identical in mice with
 A:Reference number: 149761; PMID:9429288; PMID:8026864
 A:Accession: 149761
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-641 <RES>
 A:Cross-references: UNIPROT:P16627; GB:I27086; NID:g457299; PIDN:AAA5362.1; PID:g457300
 C:Genetics:
 A:Gene: Hsc70c
 C:Function:
 A:Description: involved in protein folding and assembling/dissassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 5.2%; Score 90.5; DB 2; Length 641;
 Best Local Similarity 26.6%; Pred. No. 2.9;
 Matches 25; Conservative 16; Mismatches 38; Indels 15; Gaps 2;

QY 234 TMVLEFKCKHSPKFNENCLPHHQCPRRLSSAAPVGLTSHQYHNPISHVSG 293
 DB 241 SHFVEEFKKKKKDDISQNRAY-----RRLRTACERAKRTLSSTQANLEISLVEG 292
 QY 294 VDFYSELRNKGFQ-----RGASQELKAVRS 320
 DB 293 IDFTSITRARPFEELCADLFRGLTLEPVEKSLRDA 326

RESULT 10
 T07620
 dnaK-type molecular chaperone hsp70 - Cyanophora paradoxa (fragment)
 C:Species: Cyanophora paradoxa
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C:Accession: T07620
 R:Remaing, S.A.; Obidilk, P.; Rober-Kleber, N.; Mueller, S.B.; Hofmann, C.J.; van de Pee
 Bur, J. Physiol. 32, 279-285, 1997
 A:Title: Molecular phylogeny of the stress-70 protein family with certain emphasis on al
 A:Reference number: Z16057
 A:Accession: T07620
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-465 <REN>
 A:Cross-references: UNIPROT:P93662; EMBL:X80949
 C:Genetics:
 A:Gene: hsp70
 C:Function:
 A:Description: involved in protein folding and assembling/dissassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 5.1%; Score 89.5; DB 2; Length 465;
 Best Local Similarity 24.8%; Pred. No. 2.5;
 Matches 33; Conservative 17; Mismatches 40; Indels 43; Gaps 4;

QY 195 NIGPEDMRPHVWNYGMAFYMAWLSFTCCMASAVTTNTYTRMVLKFKCKHSPKFNPC 254
 DB 48 HLGGEFDPRMNY-----FQGEKKKKKKDKMSGNRA 80
 QY 255 LPHHQCPRRLSSAAPVGLTSHQYHNPISHVSGVDYSELRNKGFQ-----R 307
 DB 81 L-----RRLRTACERAKRTLSSTQANLEISLVEGIDFVATITRAKFEELNIDLR 131
 QY 308 GASQELKAVRS 320
 DB 132 GCLPEVEKSLRDA 144

RESULT 11
 JCI391
 dnaK-type molecular chaperone 701V - sea urchin (Paracentrotus lividus)
 N:Alternate names: heat shock protein 701V; hsp701V protein
 C:Species: Paracentrotus lividus (common urchin)
 C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 09-Jul-2004

C:Accession: JCI391
 R:Scanzo, G.; Scardina, G.; Ferraro, M.G.
 Gene 121, 353-358, 1992
 A:Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70
 A:Reference number: JCI391; PMID:93077053; PMID:1339375
 A:Accession: JCI391
 A:Molecule type: DNA
 A:Residues: 1-639 <SCO>
 A:Cross-references: UNIPROT:Q06248; EMBL:X61379; NID:g312916; PIDN:CAA4365.1; PID:g3129
 C:Genetics:
 A:Gene: hsp701V
 A:introns: 61/2
 C:Function:
 A:Description: involved in protein folding and assembling/dissassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 5.1%; Score 89; DB 2; Length 639;
 Best Local Similarity 31.9%; Pred. No. 4;
 Matches 22; Conservative 10; Mismatches 29; Indels 8; Gaps 1;

QY 238 LFFCKHSPKFNENCLPHHQCPRRLSSAAPVGLTSHQYHNPISHVSGVDY 297
 DB 243 LFFKKRYKKDKMTNPRAL-----RRLRTACERAKRTLSSTQANLEISLVEGIDY 294
 QY 298 SELRNKGFQ 306
 DB 295 TISIRARPE 303

RESULT 12
 I54542
 dnaK-type molecular chaperone HSP70 - rat
 N:Alternate names: dnaK-type molecular chaperone HSP70D; heat shock protein 70
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I54542; I68986; S43388; S47522; I56574; S35955; S38199; S41413; S41414
 R:Palmer, L.; Rauh, F.; Gunther, B.
 Immunogenetics 40, 325-330, 1994
 A:Title: Comparative analysis of the three major histocompatibility complex-linked heat
 A:Reference number: I54542; PMID:95012453; PMID:7927536
 A:Accession: I54542
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-641 <MAL1>
 A:Cross-references: UNIPROT:Q07439; UNIPROT:Q63256; EMBL:X77207; NID:g1814000; PIDN:CAA5
 A:Experimental source: HSP70.1
 A:Genetics: HSP1
 A:Accession: I68986
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-641 <MAL2>
 A:Cross-references: EMBL:X77208; NID:g927512; PIDN:CAA54423.1; PID:g450932
 A:Experimental source: HSP70.2
 A:Genetics: HSP2
 R:Kestirli, R.; Chi, S.H.; Sayen, M.R.; Dillmann, W.H.
 Biochem. J. 298, 561-569, 1994
 A:Title: Isolation of a novel inducible rat heat-shock protein (HSP70) gene and its expr
 A:Reference number: S43388; PMID:94190258; PMID:8141767
 A:Accession: S43388
 A:Molecule type: DNA
 A:Residues: 1-670, 'NG', '73-109', 'K', '111-203', 'R', '205-261', 'P', '263', 'ADGV', '268-641 <MES>
 A:Cross-references: EMBL:X75357; NID:g407163; PIDN:CAA51140.1; PID:g407164
 A:Experimental source: Ischaemic rat heart
 R:Liowski, K.; Widlak, W.; Krawczyk, Z.; Wolniczke, P.; Wisniewski, J.
 Biochim. Biophys. Acta 1219, 64-72, 1994
 A:Title: Cloning, nucleotide sequence and expression of rat heat inducible hsp70 gene.
 A:Reference number: S47522; PMID:94368874; PMID:8086479
 A:Accession: S47522
 A:Molecule type: DNA
 A:Residues: 1-70, 'NG', '73-407', 'A', '409-641 <LIS>
 A:Cross-references: EMBL:X74271; NID:g3413498; PIDN:CAA52328.1; PID:g396270
 A>Note: the authors translated the codon CCG for residue 365 as Asp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:55:46 ; Search time 102.168 Seconds
(without alignments)
1633.949 Million cell updates/sec

Title: US-10-019-151C-3
Perfect score: 1738
Sequence: 1 MAMBEISKAPSGQRTLLSAL.....RGASQELKEAVRSVSEEQ 326

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UnIProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1733	99.7	326	Q8NBR4	Q8NBR4 homo sapien
2	1718	98.8	323	Q8NBR3	Q8NBR3 homo sapien
3	1450.5	83.5	275	Q8NBS0	Q8NBS0 mus sapien
4	1249.5	71.9	365	Q8RIW2	Q8RIW2 mus musculu
5	1214.5	69.9	366	Q6AYL2	Q6AYL2 rattus norv
6	987.5	56.8	343	Q8NBR1	Q8NBR1 homo sapien
7	887.5	51.1	304	Q9Z1H7	Q9Z1H7 mus musculu
8	789.5	45.4	217	Q9D9Z3	Q9D9Z3 mus musculu
9	785.5	45.2	217	Q8C2N5	Q8C2N5 mus musculu
10	657.5	37.8	285	Q96S16	Q96S16 homo sapien
11	643.5	37.0	282	Q9BUY4	Q9BUY4 homo sapien
12	623	35.8	326	Q96LP9	Q96LP9 mus sapien
13	531	30.6	280	Q6UXI4	Q6UXI4 homo sapien
14	366	21.1	194	Q7Z6F8	Q7Z6F8 homo sapien
15	365.5	21.0	176	Q8T8B1	Q8T8B1 homo sapien
16	348	20.0	175	Q6DBD5	Q6DBD5 xenopus lae
17	111	6.4	314	Q98UH4	Q98UH4 gallus gall
18	108.5	6.2	315	CCG3 HUMAN	CCG3 HUMAN
19	108.5	6.2	328	Q90X18	Q90X18 gallus gall
20	107.5	6.2	327	CCG4 RAT	CCG4 RAT
21	106.5	6.1	327	CCG3 MOUSE	CCG3 MOUSE
22	105.5	6.0	315	CCG3 RAT	CCG3 RAT
23	104.5	6.0	607	VE1_HPV24	VE1_HPV24
24	104	6.0	203	CLDM_HUMAN	CLDM_HUMAN
25	104	6.0	327	CCG4 HUMAN	CCG4 HUMAN
26	103	5.9	512	Q8K4H0	Q8K4H0
27	102.5	5.9	250	Q8UFZ8	Q8UFZ8
28	102	5.9	323	Q99PR9	Q99PR9
29	100.5	5.8	165	1_NKG7 MOUSE	1_NKG7 MOUSE
30	100.5	5.8	275	Q6GM02	Q6GM02
31	100.5	5.8	281	CLC5_CAEEL	CLC5_CAEEL

32	100.5	5.8	323	1	CCG3 HUMAN	Q9Y698 homo sapien
33	100.5	5.8	650	2	Q9U777	Q9U777 atylophora
34	99.5	5.7	165	2	Q9CY35	Q9CY35 mus musculu
35	99.5	5.7	315	1	CCG3 MOUSE	Q9J1V5 mus musculu
36	99	5.7	191	2	Q6E568	Q6E568 fugu rubrip
37	99	5.7	323	1	CCG3 MOUSE	Q88602 mus musculu
38	99	5.7	323	2	Q71RT2	Q71RT2 rattus norv
39	98.5	5.7	190	2	Q6E5P1	Q6E5P1 fugu rubrip
40	98.5	5.7	443	2	Q6N218	Q6N218 rhodospheido
41	98	5.6	275	2	CCG3 MOUSE	Q8V410 mus musculu
42	96	5.5	275	1	CCG5 MOUSE	Q8VHW4 mus musculu
43	96	5.5	275	1	CCG5 RAT	Q8VHW4 rattus norv
44	95.5	5.5	220	1	CLDM MOUSE	Q9D7U6 mus musculu
45	95.5	5.5	324	2	Q6PFS3	Q6PFS3 brachydanto

ALIGNMENTS

RESULT 1	Q8NBR4	PRELIMINARY;	PRT;	326 AA.
AC	Q8NBR4;			
DT	01-OCT-2002 (TREMBlrel. 22, Created)			
DT	01-OCT-2002 (TREMBlrel. 22, Last sequence update)			
DT	01-OCT-2002 (TREMBlrel. 22, Last annotation update)			
DS	Hypothetical protein FLJ90841.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Isoqal T., Oca T., Nishikawa T., Hayaehi K., Otsuki T., Sugiyama T.,			
RA	Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,			
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,			
RA	Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,			
RA	Hacori A., Okumura K., Iwayanagi T., Ninomiya K.,			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK075322; BAC11548.1; -			
SQ	SEQUENCE 326 AA; 36751 MW; 9A9682984F6B6D06 CRC64;			
Query Match	99.7%; Score 1733; DB 2; Length 326;			
Best Local Similarity	99.7%; Pred. No. 4,4e-147;			
Matches 325; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
QY	1 MAMBEISKAPSGQRTLLSALISLSPSTTSLSNVYFGTQKVPKPLCEKGLAAKCPD 60			
DB	1 MAMBEISKAPSGQRTLLSALISLSPSTTSLSNVYFGTQKVPKPLCEKGLAAKCPD 60			
QY	61 MPVSLDGDINTSTQBVVQVYMETGDDRFSFRSFRSGMWLSCBETVEBGERCRSFIELTP 120			
DB	61 MPVSLDGDINTSTQBVVQVYMETGDDRFSFRSFRSGMWLSCBETVEBGERCRSFIELTP 120			
QY	121 PARREILMLSLGQITTYIGQPTISPLLLTDLTLTENPACGLSLAPAAVSSVLSGLGM 180			
DB	121 PARREILMLSLGQITTYIGQPTISPLLLTDLTLTENPACGLSLAPAAVSSVLSGLGM 180			
QY	121 PARREILMLSLGQITTYIGQPTISPLLLTDLTLTENPACGLSLAPAAVSSVLSGLGM 180			
DB	121 PARREILMLSLGQITTYIGQPTISPLLLTDLTLTENPACGLSLAPAAVSSVLSGLGM 180			
QY	181 VAHMTSVOYFOATVNLGPEDMRPHVMNYGAFYMAVLSFTCCNAAVATTTNTYTNVLEF 240			
DB	181 VAHMTSVOYFOATVNLGPEDMRPHVMNYGAFYMAVLSFTCCNAAVATTTNTYTNVLEF 240			
QY	241 KCGHSKSPKPNPCLEPHHQCFFPRRLSSAAPTGVPTSTHYQYNQPIHVSSEGVDFYSEL 300			
DB	241 KCGHSKSPKPNPCLEPHHQCFFPRRLSSAAPTGVPTSTHYQYNQPIHVSSEGVDFYSEL 300			
QY	301 RNKGFORGASQELKEAVRSVSEEQ 326			
DB	301 RNKGFORGASQELKEAVRSVSEEQ 326			
RESULT 2	Q8NBR4			

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ID 08N4M3 PRELIMINARY; PRT; 323 AA.
AC 08N4M3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GSG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCB1_TaxID=9606;
OX NCB1_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriques S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL:BC033854; AAH33854.1; -.
SQ SEQUENCE 323 AA; 36376 MW; 5FBEL3C21BF6C081 CRC64;

Query Match 98.8%; Score 1718; DB 2; Length 323;
Best Local Similarity 99.7%; Pred. No. 9,7e-146;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 MELSKAFSGQRTLLSAIILSMLSLSPSTSLISNYWVGQVKPKLCEKGLAAKCFDMPV 63
DB 1 MELSKAFSGQRTLLSAIILSMLSLSPSTSLISNYWVGQVKPKLCEKGLAAKCFDMPV 60

QY 64 SLUDGDNNTSTQEVVQYNWETGDRFSPFRSGMWLSCEETVEBERCRSFIELTPPAK 123
DB 61 SLUDGDNNTSTQEVVQYNWETGDRFSPFRSGMWLSCEETVEBERCRSFIELTPPAK 120

QY 124 REILMLSLGTQITTYIGLQPIISFLILTDLLITGNPACGLKLSAFAVSSVLSGLGMVAH 183
DB 121 REILMLSLGTQITTYIGLQPIISFLILTDLLITGNPACGLKLSAFAVSSVLSGLGMVAH 180

QY 184 MWYSQVFOATVNLGPEDMRPHVWNYGMAYMAWLSFTCCMASAVTTFTNTYRNLVEPKCK 243
DB 181 MWYSQVFOATVNLGPEDMRPHVWNYGMAYMAWLSFTCCMASAVTTFTNTYRNLVEPKCK 240

QY 244 HSKSPFKNPNCLEPHHQCPRRLSSAAPVTGPLYTHQYHNPRIHSVSGVDYSELRLNK 303
DB 241 HSKSPFKNPNCLEPHHQCPRRLSSAAPVTGPLYTHQYHNPRIHSVSGVDYSELRLNK 300

QY 304 GFQRGASQELKEAVRSVVEEOC 326
DB 301 GFQRGASQELKEAVRSVVEEOC 323

RESULT 3
Q8NBS0
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ID 08NBS0 PRELIMINARY; PRT; 275 AA.
AC 08NBS0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ90830.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCB1_TaxID=9606;
OX NCB1_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Nishikawa T., Hayaishi K., Otsuka T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahata K.,
RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aocuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nihomura K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL:AK075311; BAC11540.1; -.
SQ SEQUENCE 275 AA; 31300 MW; 503F7AC849CBEB9 CRC64;

Query Match 83.5%; Score 1450.5; DB 2; Length 275;
Best Local Similarity 84.0%; Pred. No. 8.3e-122;
Matches 274; Conservative 1; Mismatches 0; Indels 51; Gaps 1;

QY 1 MAKMELSKAFSGQRTLLSAIILSMLSLSPSTSLISNYWVGQVKPKLCEKGLAAKCFD 60
DB 1 MAKMELSKAFSGQRTLLSAIILSMLSLSPSTSLISNYWVGQVKPKLCEKGLAAKCFD 60

QY 61 MEVSLDGNNTSTQEVVQYNWETGDRFSPFRSGMWLSCEETVEBERCRSFIELTP 120
DB 61 MEVSLDGNNTSTQEVVQYNWETGDRFSPFRSGMWLSCEETVEBERCRSFIELTP 120

QY 121 PAKREILMLSLGTQITTYIGLQPIISFLILTDLLITGNPACGLKLSAFAVSSVLSGLGM 180
DB 121 PAKR-----GLGM 129

QY 181 VAHMYWYQVFOATVNLGPEDMRPHVWNYGMAYMAWLSFTCCMASAVTTFTNTYRNLVE 240
DB 130 VAHMYWYQVFOATVNLGPEDMRPHVWNYGMAYMAWLSFTCCMASAVTTFTNTYRNLVE 189

QY 241 KCKHKSFPKNPNCLEPHHQCPRRLSSAAPVTGPLYTHQYHNPRIHSVSGVDYSEL 300
DB 190 KCKHKSFPKNPNCLEPHHQCPRRLSSAAPVTGPLYTHQYHNPRIHSVSGVDYSEL 249

QY 301 RNKGFORGASQELKEAVRSVVEEOC 326
DB 250 RNKGFORGASQELKEAVRSVVEEOC 275

RESULT 4
Q8RLW2
ID 08RLW2 PRELIMINARY; PRT; 365 AA.
AC 08RLW2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag1 protein.
OS Name=Gag1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCB1_TaxID=10090;
OX NCB1_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Uaditi T.B., Toshlyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skelton U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.,
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC023009; AAH23009.1; -
 DR MGD; MGI:1194499; Gggl.
 DR GO; GO:0016021; C:Integral to membrane; TAS:
 SQ SEQUENCE 365 AA; 40612 MW; 2D0A0AEC0BA971FD CRC64;
 Query Match 71.9%; Score 1249.5; DB 2; Length 365;
 Best Local Similarity 66.3%; Pred. No. 1.3e-103;
 Matches 242; Conservative 25; Mismatches 55; Indels 43; Gaps 3;
 QY 4 MELSKAFSGQRTLLSAILSMLSLSPSTLSLNYWFGVQKVPKPLCEKGLAAKCFDMPV 63
 DB 1 MEFQKSSDQRTFVSAIINMLSLGLSTASLSSSEMFVGAQKVPKPLCGQSLAAKCFDMPM 60
 QY 64 SLQGD-TNISTQVQVQWNETGDDRRFSFRSGMMLSCBETVEBPERCRSPTELP 122
 DB 61 SLQGIANTSAQVQWYTWETGDDRRFSFLAFRSGMMLSCBETVEBPERCRSPTELP 120
 QY 123 KR-----ELIWSLGTQITTYGLQ 141
 DB 121 QREKGLBEPATLQSGCHPTLRFGGEWLMERKASLIHPMGVAVKVPWLSLGAQTAIYGLQ 180
 QY 142 FISFLLLTDLLLTGNPACGLKLSAPAAVSSVLSGLGVAHMMYQVFOATVNLGPE 201
 DB 181 LISFLLLTDLLLTNNGCGGLKLSAPAAVSLVLSGLGVAHMLYQVFOATVNLGPE 240
 QY 202 RPHVNYGMAFYAAWLSFTCCMASAVTTTNTTNTMTLEFKCKSKSKPKENPCLPHHOC 261
 DB 241 RPHSNWYGAFFYAAWLSFTCCMASAVTTTNTTNTMTLEFKCKSKSKPKENPCLPHHOC 300
 QY 262 F-FPRLSSAAPVYGLTSYHGYHNOPIHVSSEGVDFPSLBNKSGFORGASOELKEAVRSS 320
 DB 301 FLPPPLCTTHAGBPLSSCHQPSHPIRSVSEALDLYSALQDKXFOQISQELKEAVRSS 360
 QY 321 VEEBOC 325
 DB 361 VEEBOC 365
 RESULT 5
 Q6AYL2 PRELIMINARY; PRT; 366 AA.
 AC Q6AYL2;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Hypochemical protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marzula K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uaditi T.B., Toshlyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skelton U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC079000; AAH79000.1; -
 DR KW Hypochemical protein.
 SQ SEQUENCE 366 AA; 40559 MW; 20807F1B9567C494 CRC64;
 Query Match 69.9%; Score 1214.5; DB 2; Length 366;
 Best Local Similarity 65.4%; Pred. No. 1.8e-100;
 Matches 240; Conservative 22; Mismatches 60; Indels 45; Gaps 4;
 QY 4 MELSKAFSGQRTLLSAILSMLSLSPSTLSLNYWFGVQKVPKPLCEKGLAAKCFDMPV 63
 DB 1 MEFQKSSDQRTFVSAIINMLSLGLSTASLSSSEMFVGAQKVPKPLCGQSLAAKCFDMPM 60
 QY 64 SLQGD-TNISTQVQVQWNETGDDRRFSFRSGMMLSCBETVEBPERCRSPTELP 122
 DB 61 SLQGIANTSAQVQWYTWETGDDRRFSFLAFRSGMMLSCBETVEBPERCRSPTELP 120
 QY 123 KR-----ELIWSLGTQITTYGLQ 141
 DB 121 QREKGLBEPATLQSGCHPTLRFGGEWLMERKASLIHPMGVAVKVPWLSLGAQTAIYGLQ 180
 QY 142 FISFLLLTDLLLTGNPACGLKLSAPAAVSSVLSGLGVAHMMYQVFOATVNLGPE 201
 DB 181 LISFLLLTDLLLTNNGCGGLKLSAPAAVSLVLSGLGVAHMLYQVFOATVNLGPE 240
 QY 202 RPHVNYGMAFYAAWLSFTCCMASAVTTTNTTNTMTLEFKCKSKSKPKENPCLPHHOC 261
 DB 241 RPHSNWYGAFFYAAWLSFTCCMASAVTTTNTTNTMTLEFKCKSKSKPKENPCLPHHOC 300
 QY 262 F-FPRLSSAAPVYGLTSYHGYHNOPIHVSSEGVDFPSLBNKSGFORGASOELKEAVRSS 319
 DB 301 FLPPPLCTTHAGBPLSSCHQPSHPIRSVSEALDLYSALQDKXFOQISQELKEAVRSS 360
 QY 320 VEEBOC 326
 DB 361 SV-EEBOC 366
 RESULT 6
 Q8BNT1 PRELIMINARY; PRT; 343 AA.
 AC Q8BNT1;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Hypochemical protein (human).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

OX NCHI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai S., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuma S., Sasaki N.,
RA Hattori A., Okumura K., Iwanagi T., Nishimura K.,
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075288; BAC11524.1; -.
DR Genem; HGNC:19716; GSG1.
SQ SEQUENCE 343 AA; 38154 MW; F71938F7435C3FC2 CRC64;

Query Match 56.8%; Score 987.5; DB 2; Length 343;
Best Local Similarity 61.9%; Pred. No. 4e-80;
Matches 226; Conservative 13; Mismatches 65; Indels 61; Gaps 13;

QY 1 MAKMEISKAFSGQRTLLSAILSMLSLSPFTTSLSNYFWVGQKPKLCEKGLAKCFD 60
DB 1 MAKMEISKAFSGQRTLLSAILSMLSLSPFTTSLSNYFWVGQKPKLCEKGLAKCFD 60
QY 61 MPVSLDGDNTSTQEVVQYNNMETGDDRFSFRSPRSGMWLSCSEETVEBGERCRSFIELTP 120
DB 61 MPVSLDGDNTSTQEVVQYNNMETGDDRFSFRSPRSGMWLSCSEETVEBGERCRSFIELTP 120
QY 121 PARREILMLSLGQIYYIGLQFISFILLLTDLLLTGNPACGLKLSAFAVSVLSGLLG- 179
DB 121 PARRGEKGL-----LEFATLQGPCHPTLPFG---GKRLMEKASLPSPPLGLCGK 166
QY 180 --MVA-----HMVYSGVFQ---ATVNLGPEDMRPHVWNYGMAYMWLSTFCMASAVTT 229
DB 167 NPVIVTGNADHLHRTSTHQLPATNRLATN-WEPCW-----AQTERLCCCFELCPVNS 218
QY 230 -----PNTYTRNV-----LEFKC-----KHSKS---FKENPNC--LPH-HHQC 261
DB 219 PGDGPDPVFTSLPSCDQLGSRRLFTTCLEMLGLGLALHLHLHGVCCHLQHVHHQC 278
QY 262 PPRRLSSAAPTVGPLTSHYOHNOPIHSEGVDFPYSSELNKGFORGASDELKAVRSSV 321
DB 279 PPRRLSSAAPTVGPLTSHYOHNOPIHSEGVDFPYSSELNKGFORGASDELKAVRSSV 338
QY 322 EEEQC 326
DB 339 EEEQC 343

RESULT 7
Q921H7 PRELIMINARY; PRT; 304 AA.
AC Q921H7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GSG1.
DE Name=Gsg1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Black 6; TISSUE=Testis;
RX MEDLINE=95046372; PubMed=7957958; DOI=10.1016/0014-5793(94)01155-9;
RA Tanaka H., Yoshimura Y., Nishina Y., Nozaki M., Nojima H.,
RA Nishimune Y.,
RA "Isolation and characterization of cDNA clones specifically expressed
RT in testicular germ cells."
RL FEBS Lett. 355:4-10(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Black 6; TISSUE=Testis;
RX MEDLINE=98051916; PubMed=9337410;
RA Matsui M., Ichihara H., Kobayashi S., Tanaka H., Tsuchida J.,

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RA Nozaki M., Yoshimura Y., Nojima H., Rochelle J.M., Nishimune Y.,
RA Takeo M.M., Seldin M.F.;
RT "Mapping of six germ-cell-specific genes to mouse chromosomes.";
RL Mamm. Genome 8:873-874(1997).
DR EMBL; D87325; BAA37087.1; -.
DR MGD; MGI:1194499; Gsg1.
DR GO; GO:0016021; C:integral to membrane; TAS.
SQ SEQUENCE 304 AA; 33454 MW; 8B19F6F1CAAB5016 CRC64;

Query Match 51.1%; Score 887.5; DB 2; Length 304;
Best Local Similarity 61.3%; Pred. No. 3.3e-71;
Matches 185; Conservative 17; Mismatches 45; Indels 55; Gaps 5;

QY 4 MELSFAFGQRTLLSAILSMLSLSPFTTSLSNYFWVGQKPKLCEKGLAKCFDMPV 63
DB 1 MEFQKSSDQKRTFISLILMLSLGISTSLSEFWVGQKPKLCEKGLAKCFDMPV 60
QY 64 SLDDG-DTNTSTQEVVQYNNMETGDDRFSFRSPRSGMWLSCSEETVEBGERCRSFIELTP 122
DB 61 SLDDGANTSNABVQYTWETGDDRFSFLAFPSGMWLSCEETMEBGERCRSFIELTP 120
QY 123 KR-----ELMLSLGQIYYIGLQ 141
DB 121 QREKGLLEFATLQSGCHPTLPFGGEWLMKASLHLPLPWGPAKYFWMLSGQIYYIGLQ 180
QY 142 FISFILLLTDLLLTGNPACGLKLSAFAVSVLSGLLGVAHMYSGVQATVNLGPE-- 199
DB 181 LISFILLLTDLLLTGNPACGLKLSAFAVSVLSGLLGVAHMYSGVQATVNLGPE 240
QY 200 ----DMRPHVWNYGMAYMWLSTFCMASAVTTENTYTRVLEFKCRKSKSPKENPCL 255
DB 241 TLLLELR-----LGLHSGVFLHL--LHGVTYTTNMTTRVVLBFKCRKSKSFNTNPCL 293
QY 256 PH 257
DB 294 AH 295

RESULT 8
Q9J9Z3 PRELIMINARY; PRT; 217 AA.
AC Q9J9Z3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:170025C22 product:germ cell-specific gene 1, full
DE insert sequence.
DE Name=Gsg1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RA "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of

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RT 60, 770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoaka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
 RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata A., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK006326; BAB24527.1; -.
 DR MGD; MGI:1194499; Gsg1.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 SO SEQUENCE 217 AA; 24215 MW; C9775AC6478AF1B CRC64;
 Query Match 45.4%; Score 789.5; DB 2; Length 217;
 Best Local Similarity 72.9%; Pred. No. 1.4e-62;
 Matches 151; Conservative 15; Mismatches 38; Indels 3; Gaps 2;
 QY 120 PPAKELIMSLGCTQTYIGQPSILLTDLITGNPACGLGSAFAVSVLGLG 179
 DB 13 PVAK-VFWLSTLAQTYIGQLISFLITLTLTDPGGLDLSAFAVSVLGLG 70
 QY 180 MVAHMYSGVFOATVNLGPEDMRPVWNYGAFYMAVLSFTCCASAVTTFTTTRVLE 239
 DB 71 MVAHMYSGVFOATVNLGPEDMRPVWNYGAFYMAVLSFTCCASAVTTFTTTRVLE 130
 QY 240 FKCKHSKSPKPNPCLEPHHQCPR-PRRLSSAAPTGVPLTGYHQYNOPRHSVSEGVDFYS 298
 DB 131 FKCKHSKSPKPNPCLEPHHQCPR-PRRLSSAAPTGVPLTGYHQYNOPRHSVSEGVDFYS 130
 QY 299 ELANKGPGRGAQGLKKAFAVSSVBEQ 325
 DB 191 ALDDKEPQGGISQELKEVPSVEEOR 217

DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
 DE length enriched library, clone:R430010020 product:germ cell-specific
 DE gene 1, full insert sequence.
 GN Name=Gsg1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RA The PANTOM Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hayashizaki Y.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirazane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kaga I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata A., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takasu-Akahira S., Takada Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Yasunishi M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK088285; BAC40258.1; -.
 DR MGD; MGI:1194499; Gsg1.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 SO SEQUENCE 217 AA; 24197 MW; CD371DE7B7156F1B CRC64;

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
 RA Kravinsky M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC001796; AA01796.1; - F0F7D123255A2935 CRC64;

SO SEQUENCE 282 AA; 31102 MW; 10F7D123255A2935 CRC64;

Query Match 37.0%; Score 643.5; DB 2; Length 282;

Best Local Similarity 51.1%; Pred. No. 2.5e-49;

Matches 162; Conservative 14; Mismatches 76; Indels 65; Gaps 11;

QY 4 MELSKAPSGORTLSAIIISLMSLSFSTTSLSNYPVGTOKYKPKLCEKGLAKCFDMPV 63
 DB 1 MELSKAPSGORTLSAIIISLMSLSFSTTSLSNYPVGTOKYKPKLCEKGLAKCFDMPV 60

QY 64 SLDDGNTSTQEVVQYNNMETGDRSPFRSGMWLSCEETVBERPALLHPQSKPRL 123
 DB 61 SLDDGNTSTQEVVQYNNMETGDRSPFRSGMWLSCEETVBERPALLHPQSKPRL 120

QY 124 REILWLSLGTQITTYIGLOFISFLLLTDLTLGNPAAGLISAPAAVSVLSGLG--M 180
 DB 121 RGEKGL-----LEFATLQGPCHPTLRFG---GKILMEKASLPSPPLGCGKNPM 166

QY 181 VA-----HMYTGVQF---ATVALGPEQWPRHYVNTGMAFYAMLSFTCCMASAVTTTNT 232
 DB 167 VLPGNADHLHRTSIHQLPATNRLATH-WEPCILM-----AQTERLCCC----- 208

QY 233 YTRMVLFPKCKISKSKFKNPN-----CLPHHOCPPRLSAA-----PTVGPITSYHQ-- 281
 DB 209 -----FLCPVRSRGGDGPVFTSLPSCQLGSRRLTCLIELMLGLHGLALLHLH 261

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

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 DB 262 GVGCHLQHVDGAGV 278

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 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 282 ----YHNPRIHSVSGV 294
 DB 262 GVGCHLQHVDGAGV 278

QY 3 KMLSKAPSGORTLSAIIISLMSLSFSTTSLSNYPVGTOKYKPKLCEKGLAKCFDMP 62
 DB 16 MELSKAPSGORTLSAIIISLMSLSFSTTSLSNYPVGTOKYKPKLCEKGLAKCFDMP 75

QY 63 VSLDDGNTSTQEVVQYNNMETGDRSPFRSGMWLSCEETVBERPALLHPQSKPRL 108
 DB 76 VSLDDGNTSTQEVVQYNNMETGDRSPFRSGMWLSCEETVBERPALLHPQSKPRL 135

QY 109 -----GECRSFIELTPPAKREILWLSLGTQITTYIGLOFISFLLLTDLTLGNPA 159
 DB 136 RSSGTAAGRCRSPFIELTPPAKRGKGL-----LEFATLQGPCHPTLRFG--- 182

QY 160 CGIKLSAPAAVSVLSGLG---MVA-----HMYTGVQF---ATVALGPEQWPRHYVNT 208
 DB 183 -GRILMEKASLPSPPLGCGKNPMVLPGNADHLHRTSIHQLPATNRLATH-WEPCILM-- 238

QY 209 GMAFYAMLSFTCCMASAVTTTNTYTRMVLFPKCKISKSKFKNPN-----CLPHHOCPPR 264
 DB 239 -----AQTERLCCC-----FLCPVRSRGGDGPVFTSLPSCQLGSRRLTCLIELMLGLHGLALLHLH 276

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

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 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

QY 265 RLSSAA-----PTVGPITSYHQ-----YHNPRIHSVSGV 294
 DB 277 RLTTCLIELMLGLHGLALLHLHGVCHLQHVDGAGV 317

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QY 177 LIGVAVHMYSOVFOATVNLGPEDMRPHVWNYGMAYFAMVLSPTCCMASAVTTNTYTM 236
DB 134 LIGVAVHMYTVOFQVTVSLGPEDMRPHSHWDGMSFCLAMGSPCCMAASVTTLNTYTK 193
QY 237 VLEPKCKH---SKSPKENDPNCU-----PH 257
DB 194 VLEPRKRKRVFEGYREBEPTFIDPEAIKVFREMERKRDSEEDPHLDCHERYPARHQPH 253
QY 258 HHQCFPRRLSSAP 271
DB 254 MADSWPRSSAOEAP 267

RESULT 14
QY 0726F8 PRELIMINARY; PRT; 194 AA.
AC 0726F8;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE MGCI8079.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li H., Li S., Zhou C., Shen C., Li M., Xiao W., Lin L., Yang S.;
RA Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY302134; AAP57626.1; -.
SQ SEQUENCE 194 AA; 22738 MW; 3B0AB145D1FAB663 CRC64;

Query Match 21.1%; Score 366; DB 2; Length 194;
Best Local Similarity 44.6%; Pred. No. 1.3e-24;
Matches 83; Conservative 30; Mismatches 61; Indels 12; Gaps 6;

QY 151 DLLTGNPACGLKLSAPAVSVLSGLGVMVAMMYSOVFOATVNLGPEDMRPHVWNYGM 210
DB 4 ELPHSSNVTDGKLNAFAVFTVLSGLGVMVAMMYTVOFQVTVSLGPEDMRPHSHWDG 63
QY 211 AFYMAVLSPTCCMASAVTTNTYTMVLEPKCKH---SKSPKENDPNCU---PHHQCFPRRL 266
DB 64 SFCLAMGSPCCMAASVTTLNTYTKVIEFRKRKRVFEGYREBEPTFIDPEAIKVFREMR 123
QY 267 SSAAPVGLTSTHYQHNPISHVSGVDPYSFLRKKGQKASQSLKKA-VRSSVE-- 323
DB 124 QIEAQR-GRATCPRSHWMEKDGSE-EDFHLDCRHERYPARHQPHMADSWPRSSAOEAP 181
QY 324 ---EQC 326
DB 182 ELNRQC 187

RESULT 15
QY 08TB81 PRELIMINARY; PRT; 176 AA.
AC 08TB81;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein MGCI8079.
GN Name=MGCI8079;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RA Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016460; AAH16460.1; -.
KW Hypothetical protein.
SQ SEQUENCE 176 AA; 20586 MW; 408A16130B3F252C CRC64;

Query Match 21.0%; Score 365.5; DB 2; Length 176;
Best Local Similarity 45.0%; Pred. No. 1.3e-24;
Matches 72; Conservative 21; Mismatches 28; Indels 39; Gaps 2;

QY 151 DLLTGNPACGLKLSAPAVSVLSGLGVMVAMMYSOVFOATVNLGPEDMRPHVWNYGM 210
DB 4 ELPHSSNVTDGKLNAFAVFTVLSGLGVMVAMMYTVOFQVTVSLGPEDMRPHSHWDG 63
QY 211 AFYMAVLSPTCCMASAVTTNTYTMVLEPKCKH---SKSPKENDPNCU----- 255
DB 64 SFCLAMGSPCCMAASVTTLNTYTKVIEFRKRKRVFEGYREBEPTFIDPEAIKVFREMR 123
QY 256 -----PHHQCFPRRLSSAP 271
DB 124 EKRDSEEDPHLDCHERYPARHQPHMADSWPRSSAOEAP 163

Search completed: July 14, 2005, 20:32:20
Job time : 109.168 secs

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